



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 111937

TO: Jeanine Goldberg
Location: cm1/12d11
Art Unit: 1634
Tuesday, January 13, 2004

Case Serial Number: 10/035978

From: Barb O'Bryen
Location: Biotech-Chem Library
CM1-6A05
Phone: 308-4291

barbara.obryen@uspto.gov

Search Notes

Jeanine,
Seq 126 is 105nt long, so I didn't use the suggested length limitation for the Registry search (there were only 6 hits).

Barb

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

DM nucleic - nucleic search, using sw model
Run on: January 12, 2004, 22:35:58 : Search time 2659 seconds
(without alignments)
1615.461 Million cell updates/sec

Title: US-10-035-978A-126
Perfect score: 105
Sequence: 1 cccttagttctcgcctt.....attccagccattgttggggg 105

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_cm.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_on.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vi.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_mus.*
34: em_htg_pln.*
35: em_htg_rtd.*
36: em_htg_nam.*
37: em_htg_vrt.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	105	100.0	105	1	HPY390718
2	105	100.0	105	1	HPY390719
3	105	100.0	105	6	BD009534 Probes, m
4	105	100.0	105	6	BD009535 Probes, m
5	105	100.0	223	1	AB057126 Helicobac
6	103.4	98.5	105	1	HPY390720
7	103.4	98.5	105	6	BD009536 Probes, m
8	101.8	97.0	105	1	HPY390721
9	101.8	97.0	105	6	BD009540 Probes, m
10	101.8	97.0	223	1	AB057113 Helicobac
11	101.8	97.0	223	1	AB057141 Helicobac
12	101.8	97.0	223	1	AB057158 Helicobac
13	101.8	97.0	256	1	AF050377 Helicobac
14	101.8	97.0	631	1	AF091830 Helicobac
15	100.2	95.4	105	1	HPY390723
16	100.2	95.4	105	1	HPY390724
17	100.2	95.4	105	1	HPY390726
18	100.2	95.4	105	6	BD009537
19	100.2	95.4	105	6	BD009539 Probes, m
20	100.2	95.4	105	6	BD009541 Probes, m
21	100.2	95.4	223	1	AB057114 Helicobac
22	100.2	95.4	223	1	AB057118 Helicobac
23	100.2	95.4	223	1	AB057119 Helicobac
24	100.2	95.4	223	1	AB057132 Helicobac
25	100.2	95.4	223	1	AB057137 Helicobac
26	100.2	95.4	223	1	AB057148 Helicobac
27	100.2	95.4	223	1	AB057153 Helicobac
28	100.2	95.4	223	1	AB057159 Helicobac
29	100.2	95.4	223	1	AB057162 Helicobac
30	100.2	95.4	223	1	AB057165 Helicobac
31	100.2	95.4	631	1	AF091829 Helicobac
32	100.2	95.4	631	1	AF091833 Helicobac
33	100.2	95.4	4195	1	AF049629 Helicobac
34	100.2	95.4	4196	1	AF049640 Helicobac
35	100.2	95.4	4207	1	AF049631 Helicobac
36	100.2	95.4	4225	1	AF049641 Helicobac
37	100.2	95.4	4724	1	AF049642 Helicobac
38	99.4	94.7	105	1	HPY390725
39	99.4	94.7	105	6	BD009538 Probes, m
40	98.8	94.1	251	1	AF035614 Helicobac
41	98.6	93.9	105	1	HPY390716
42	98.6	93.9	105	1	HPY390717
43	98.6	93.9	105	6	BD009544 Probes, m
44	98.6	93.9	105	6	BD009545
45	98.6	93.9	176	6	BD009451 Probes, m

ALIGNMENTS

RESULT 1
HPY390718
LOCUS Helicobacter pylori partial vacA gene for vacA protein, isolate
DEFINITION
ACCESSION AJ390718
VERSION AJ390718.1 GI:6634382
KEYWORDS vacA gene; VacA protein.
SOURCE Helicobacter pylori
ORGANISM Helicobacter pylori
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
REFERENCE 1
AUTHORS van Doorn, L.J., Figueiredo, C., Sanna, R., Pena, S., Midolo, P.,
Ng, E.K., Atherton, J.C., Blaser, M.J. and Quint, W.G.

Pred. No. is the number of results predicted by chance to have a

TITLE Expanding allelic diversity of *Helicobacter pylori* vacA
J. Clin. Microbiol. 36 (9), 2597-2603 (1998)

98371029

PUBMED 3705399

REFERENCE 2 (bases 1 to 105)

AUTHORS van Doorn, L.J.

TITLE Direct Submission

JOURNAL Submitted (21-OCT-1999) van Doorn L.J., Molecular Biology, Delft Diagnostic Laboratory, R. de Graafweg 7, Delft, 2625 AD, NETHERLANDS

FEATURES Location/Qualifiers

source

1..105

/organism="Helicobacter pylori"

/mol_type="genomic DNA"

/isolate="JA3"

/db_xref="taxon:210"

/country="Japan"

1..105

/gene="vacA"

<1..>105

/gene="vacA"

/function="cytotoxin"

/note="g-region"

/codon_start=2

/transl_table=11

/product="VacA protein"

/protein_id="CAB64432.1"

/db_xref="GI:6634383"

/translation="PLVSLALVGLVLSITPKSHAFFTTVIIPAIVGG"

22 a 27 c 22 g 34 t

BASE COUNT

ORIGIN

Query Match 100.0%; Score 105; DB 1; Length 105;

Best Local Similarity 100.0%; Pred. No. 3.2e-23;

Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTTTAGTTTCTCGCTTTAGTGGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60

Db 1 CCCTTTAGTTTCTCGCTTTAGTGGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60

Qy 61 TGCTGCCCTTTTACACCGTGATCATTCAGCCATTGTTGGGG 105

Db 61 TGCTGCCCTTTTACACCGTGATCATTCAGCCATTGTTGGGG 105

RESULT 2

HPY390719

LOCUS

DEFINITION *Helicobacter pylori* partial vacA gene for vacA protein, isolate

HPY390719 105 bp DNA linear BCT 22-DEC-1999

HK43.

ACCESSION AJ390719

VERSION AJ390719.1 GI:6634384

KEYWORDS vacA gene; vacA protein.

SOURCE *Helicobacter pylori*

ORGANISM *Helicobacter pylori*

Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;

Helicobacteraceae; *Helicobacter*.

REFERENCE 1

AUTHORS

van Doorn, L.J., Figueiredo, C., Sanna, R., Pena, S., Midolo, P.,

Ng, E.K., Atherton, J.C., Blaser, M.J. and Quint, W.G.

Expanding allelic diversity of *Helicobacter pylori* vacA

J. Clin. Microbiol. 36 (9), 2597-2603 (1998)

98371099

PUBMED 9705399

REFERENCE 2 (bases 1 to 105)

AUTHORS van Doorn, L.J.

TITLE Direct Submission

JOURNAL Submitted (21-OCT-1999) van Doorn L.J., Molecular Biology, Delft

Diagnostic Laboratory, R. de Graafweg 7, Delft, 2625 AD,

NETHERLANDS

FEATURES Location/Qualifiers

1..105

/organism="Helicobacter pylori"

source

Qy

1 CCCTTTAGTTTCTCGCTTTAGTGGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60

Db 1 CCCTTTAGTTTCTCGCTTTAGTGGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60

Qy 61 TGCTGCCCTTTTACACCGTGATCATTCAGCCATTGTTGGGG 105

Db 61 TGCTGCCCTTTTACACCGTGATCATTCAGCCATTGTTGGGG 105

/mol_type="genomic DNA"
/isolate="HK43"
/db_xref="taxon:210"
/country="China: region Hong Kong"
1..105
/gene="vacA"
<1..>105
/gene="vacA"
/function="cytotoxin"
/note="g-region"
/codon_start=2
/transl_table=11
/product="vacA protein"
/protein_id="CAB64554.1"
/db_xref="GI:6634385"
/translation="PLVSLALVGLVLSITPKSHAFFTTVIIPAIVGG"
22 a 27 c 22 g 34 t
BASE COUNT
ORIGIN

Query Match 100.0%; Score 105; DB 1; Length 105;

Best Local Similarity 100.0%; Pred. No. 3.2e-23;

Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTTTAGTTTCTCGCTTTAGTGGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60

Db 1 CCCTTTAGTTTCTCGCTTTAGTGGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60

Qy 61 TGCTGCCCTTTTACACCGTGATCATTCAGCCATTGTTGGGG 105

Db 61 TGCTGCCCTTTTACACCGTGATCATTCAGCCATTGTTGGGG 105

RESULT 3

BD009534

LOCUS

DEFINITION

Probes, methods and kits for detection and typing of *Helicobacter*

pylori, nucleic acids in biological samples.

BD009534 105 bp DNA linear PAT 31-JAN-2002

ACCESSION BD009534.1 GI:18637907

VERSION JP 2001502536-A/126.

KEYWORDS unclassified

SOURCE unclassified

ORGANISM unclassified.

REFERENCE 1 (bases 1 to 105)

AUTHORS Quint, W. and Doorn, L.J.V.

Probes, methods and kits for detection and typing of *Helicobacter*

pylori nucleic acids in biological samples

Patent: JP 2001502536-A 126 27-FEB-2001;

INNOGENETICS NV, DBL BV

COMMENT

OS Unclassified

PN JP 2001502536-A/126

PD 27-FEB-2001

PF 10-OCT-1997 JP 1998518004

PR 16-OCT-1996 EP 96870131.8

PI WILHELMUS QUINT LEENDERT JAN VAN DOORN

PC C1Q1/68,C07K14/205,C12N15/11

CC FH

FT Key Location/Qualifiers

source 1..105

/organism="Unidentified"

/mol_type="genomic DNA"

/db_xref="taxon:32644"

22 a 27 c 22 g 34 t

BASE COUNT

ORIGIN

Query Match 100.0%; Score 105; DB 6; Length 105;

Best Local Similarity 100.0%; Pred. No. 3.2e-23;

Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1 CCCTTTAGTTTCTCGCTTTAGTGGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60

```

Db      1  CCCTTTAGTTCTCTCGCTTTAGTGGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
QY      61  TGCTGCTCTTTTACACCGTGATCATTCACGCCATTGTTGGGG 105
Db      61  TGCTGCTCTTTTACACCGTGATCATTCACGCCATTGTTGGGG 105

RESULT 4
LOCUS   BD009535
DEFINITION Probes, methods and kits for detection and typing of Helicobacter
          pylori, nucleic acids in biological samples.
ACCESSION BD009535
VERSION   1 GI:18637908
KEYWORDS JP 2001502536-A/127.
SOURCE   unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 105)
AUTHORS Quint, W. and Doorn, L.J.V.
TITLE    Probes, methods and kits for detection and typing of Helicobacter
          pylori, nucleic acids in biological samples
JOURNAL  Patent: JP 2001502536-A 127 27-FEB-2001;
          INNOGENETICS NV, DDL BV
COMMENT  OS Unidentified
          PN JP 2001502536-A/127
          PD 27-FEB-2001
          PF 10-OCT-1997 JP 1998518004
          PR 16-OCT-1996 EP 96870131.8
          PI WILHELMUS QUINT, LEENDERT JAN VAN DOORN
          PC C12Q1/68, C07K14/205, C12N15/11
          CC
          FH Key Location/Qualifiers
          FT source 1..105
          FT /organism='Unidentified'.

FEATURES
source
Location/Qualifiers
1..105
/mol_type='genomic DNA'
/db_xref='taxon:32644'
22 a 22 g 22 g 34 t

Query Match 100.0%; Score 105; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.2e-23;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CCCTTTAGTTCTCTCGCTTTAGTGGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
b 1 CCCTTTAGTTCTCTCGCTTTAGTGGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
Y 61 TGCTGCTCTTTTACACCGTGATCATTCACGCCATTGTTGGGG 105
b 61 TGCTGCTCTTTTACACCGTGATCATTCACGCCATTGTTGGGG 105

RESULT 5
LOCUS   AB057126
DEFINITION Helicobacter pylori vacA gene for vacuolating cytotoxin, partial
          cds, signal sequence, strain:JapanK55.
ACCESSION AB057126
VERSION   1 GI:19910483
KEYWORDS JP 2001502536-A/127.
SOURCE   unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 105)
AUTHORS Quint, W. and Doorn, L.J.V.
TITLE    Probes, methods and kits for detection and typing of Helicobacter
          pylori, nucleic acids in biological samples
JOURNAL  Patent: JP 2001502536-A 127 27-FEB-2001;
          INNOGENETICS NV, DDL BV
COMMENT  OS Unidentified
          PN JP 2001502536-A/127
          PD 27-FEB-2001
          PF 10-OCT-1997 JP 1998518004
          PR 16-OCT-1996 EP 96870131.8
          PI WILHELMUS QUINT, LEENDERT JAN VAN DOORN
          PC C12Q1/68, C07K14/205, C12N15/11
          CC
          FH Key Location/Qualifiers
          FT source 1..105
          FT /organism='Unidentified'.

FEATURES
source
Location/Qualifiers
1..105
/mol_type='genomic DNA'
/db_xref='taxon:32644'
22 a 22 g 22 g 34 t

Query Match 100.0%; Score 105; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.2e-23;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CCCTTTAGTTCTCTCGCTTTAGTGGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
b 1 CCCTTTAGTTCTCTCGCTTTAGTGGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
Y 61 TGCTGCTCTTTTACACCGTGATCATTCACGCCATTGTTGGGG 105
b 61 TGCTGCTCTTTTACACCGTGATCATTCACGCCATTGTTGGGG 105

RESULT 6
LOCUS   HPX390720
DEFINITION Helicobacter pylori partial vacA gene for vacA protein, isolate
          HK51.
ACCESSION AJ390720
VERSION   1 GI:6634386
KEYWORDS vacA gene; vacA protein.
SOURCE   Helicobacter pylori
ORGANISM Helicobacter pylori
REFERENCE 1 (bases 1 to 105)
AUTHORS van Doorn, L.J., Figueiredo, C., Sanna, R., Pena, S., Midolo, P.,
          Ng, E.K., Atherton, J.C., Blaser, M.J. and Quint, W.G.
TITLE    Expanding allelic diversity of Helicobacter pylori vacA
JOURNAL  J. Clin. Microbiol. 36 (9), 2597-2603 (1998)
MEDLINE 98371099
PUBMED 9705399
REFERENCE 2 (bases 1 to 105)
AUTHORS van Doorn, L.J.
TITLE    Direct Submission
JOURNAL  Submitted (21-OCT-1999) van Doorn L.J., Molecular Biology, Delft
          Diagnostic Laboratory, R. de Graafweg 7, Delft, 2625 AD,
          NETHERLANDS
FEATURES
source
Location/Qualifiers
1..105
/organism='Helicobacter pylori'

```

```

Studies of human migration
Unpublished
2 (bases 1 to 223)
Yamaoka, Y., Gutierrez, O., Saitou, N., Kodama, T., Kim, J.G.,
Kashima, K., Ramirez, F.C., Mahachai, V., Osato, M.S. and Graham, D.Y.
Direct Submission
Submitted (09-MAR-2001) Yoshio Yamaoka, Baylor College of Medicine,
Department of Medicine; VA Medical Center (111D), 2002 Holcombe
Blvd, Houston, Texas 77030, USA (E-mail: yoshio@wt.net,
Tel: 713-790-7234, Fax: 713-790-1040)
Location/Qualifiers
1..223
/organism='Helicobacter pylori'
/mol_type='genomic DNA'
/strain='JapanK55'
/db_xref='taxon:210'
/country='Japan'
1..223
/gene='vacA'
<1..>223
/gene='vacA'
/codon_start=2
/transl_table=11
/product='vacuolating cytotoxin'
/protein_id='BAB87493.1'
/db_xref='GI:19910484'
/translation='PLVSLALVGLVLSITPKSHAAFTTIIPIAVGGIATGAAGVT
VSGLLGLKQAEBAKTPDKPKVRIQA'
BASE COUNT 56 a 54 c 55 g 58 t
ORIGIN

```

```

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

```

```

gene
CDS

```

```

Query Match
Best Local Similarity
Matches
Conservative
Mismatches
Indels
Gaps

```

```

QY
Db
QY
Db

```

```

RESULT 6
HPX390720
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

```

```

HPX390720
Helicobacter pylori partial vacA gene for vacA protein, isolate
HK51.
AJ390720.1 GI:6634386
vacA gene; vacA protein.
Helicobacter pylori
Helicobacter pylori
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
Helicobacteraceae; Helicobacter.
1
van Doorn, L.J., Figueiredo, C., Sanna, R., Pena, S., Midolo, P.,
Ng, E.K., Atherton, J.C., Blaser, M.J. and Quint, W.G.
Expanding allelic diversity of Helicobacter pylori vacA
J. Clin. Microbiol. 36 (9), 2597-2603 (1998)
98371099
9705399
van Doorn, L.J.
Direct Submission
Submitted (21-OCT-1999) van Doorn L.J., Molecular Biology, Delft
Diagnostic Laboratory, R. de Graafweg 7, Delft, 2625 AD,
NETHERLANDS
Location/Qualifiers
1..105
/organism='Helicobacter pylori'

```

```

/molecule="genomic DNA"
/isoate="HK51"
/db_xref="taxon:210"
/country="China: region Hong Kong"
1..105
/gene="vaca"
<1..>105
/function="cytotoxin"
/notes="s-region"
/codon_start=2
/trans_table=11
/product="Vaca protein"
/protein_id="CAB64555.1"
/db_xref="GI:6634387"
/translation="PLVSLALVGLVLSITPQKSHAAFTTIIIPVGG"

BASE COUNT      21 a  27 c  23 g  34 t
ORIGIN
Query Match      98.5%; Score 103.4; DB 1; Length 105;
Best Local Similarity 99.0%; Pred. No. 1.1e-22;
Matches 104; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCTTAGTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
    |||
Db 1 CCCTTAGTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCGCAAAAAAGTCA 60
    |||

Qy 61 TGCTGCCCTTCTTACACCGTGATCATTCAGCCATTGTTGGGG 105
    |||
Db 61 TGCTGCCCTTCTTACACCGTGATCATTCAGCCATTGTTGGGG 105
    |||

Qy 61 TGCTGCCCTTCTTACACCGTGATCATTCAGCCATTGTTGGGG 105
    |||
Db 61 TGCTGCCCTTCTTACACCGTGATCATTCAGCCATTGTTGGGG 105
    |||

RESULT 7
BD009536
LOCUS
DEFINITION
Probes, methods and kits for detection and typing of Helicobacter
pylori nucleic acids in biological samples.
ACCESSION
BD009536
VERSION
JP 2001502536-A/128.
KEYWORDS
unidentified
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 105)
AUTHORS
Quint,W. and Doorn,L.J.V.
TITLE
Probes, methods and kits for detection and typing of Helicobacter
pylori nucleic acids in biological samples
JOURNAL
Patent: JP 2001502536-A 128 27-FEB-2001;
COMMENT
INNOGENETICS NV,DDL BV
OS Unidentified
PN JP 2001502536-A/128
PD 27-FEB-2001
PF 10-OCT-1997 JP 1998518004
PR 16-OCT-1996 EP 96870131.8
PI WILHELMUS QUINT,LEENDERT JAN VAN DOORN
PC C12Q1/68,C07K14/205,C12N15/11
FH
CH
FT
FT
FT
Location/Qualifiers
1..105
/organism="Unidentified"
/organism="unidentified"
/molecule="genomic DNA"
/db_xref="taxon:32644"

BASE COUNT      21 a  27 c  23 g  34 t
ORIGIN
Query Match      98.5%; Score 103.4; DB 6; Length 105;
Best Local Similarity 99.0%; Pred. No. 1.1e-22;
Matches 104; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCTTAGTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
    |||

```

```

Db 1 CCCTTAGTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCGCAAAAAAGTCA 60
    |||
Qy 61 TGCTGCCCTTCTTACACCGTGATCATTCAGCCATTGTTGGGG 105
    |||
Db 61 TGCTGCCCTTCTTACACCGTGATCATTCAGCCATTGTTGGGG 105
    |||

RESULT 8
HPY390721
LOCUS
DEFINITION
Helicobacter pylori partial vaca gene for Vaca protein, isolate
TH8835.
ACCESSION
AJ390721
VERSION
AJ390721.1 GI:6634388
KEYWORDS
vaca gene; Vaca protein.
SOURCE
Helicobacter pylori
ORGANISM
Helicobacter pylori
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
Helicobacteraceae; Helicobacter.
REFERENCE
1
AUTHORS
van Doorn,L.J., Figueiredo,C., Sanna,R., Pena,S., Midolo,P.,
Ng,E.K., Atherton,J.C., Blaser,M.J. and Quint,W.G.
TITLE
Expanding allelic diversity of Helicobacter pylori vaca
J. Clin. Microbiol. 36 (9), 2597-2603 (1998)
MEDLINE
98371099
PUBMED
9705399
REFERENCE
2 (bases 1 to 105)
AUTHORS
van Doorn,L.J.
TITLE
Direct Submission
JOURNAL
Submitted (21-OCT-1999) van Doorn L.J., Molecular Biology, Delft
Diagnostic Laboratory, R. de Graafweg 7, Delft, 2625 AD,
NETHERLANDS
FEATURES
Location/Qualifiers
1..105
/organism="Helicobacter pylori"
/molecule="genomic DNA"
/isoate="TH8835"
/db_xref="taxon:210"
/country="Thailand"
1..105
/gene="vaca"
<1..>105
/function="cytotoxin"
/notes="s-region"
/codon_start=2
/trans_table=11
/product="Vaca protein"
/protein_id="CAB64433.1"
/db_xref="GI:6634389"
/translation="PLVSLALVGLVLSITPQKSHAAFTTIIIPVGG"

BASE COUNT      21 a  28 c  23 g  33 t
ORIGIN
Query Match      97.0%; Score 101.8; DB 1; Length 105;
Best Local Similarity 98.1%; Pred. No. 3.5e-22;
Matches 103; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCTTAGTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
    |||
Db 1 CCCTTAGTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCGCAAAAAAGTCA 60
    |||

Qy 61 TGCTGCCCTTCTTACACCGTGATCATTCAGCCATTGTTGGGG 105
    |||
Db 61 TGCTGCCCTTCTTACACCGTGATCATTCAGCCATTGTTGGGG 105
    |||

RESULT 9
BD009540
LOCUS
DEFINITION
Probes, methods and kits for detection and typing of Helicobacter
pylori nucleic acids in biological samples.

```

```

ACCESSION      BD009540
VERSION         GI:18637913
KEYWORDS        JP 2001502536-A/132.
SOURCE          unidentified
ORGANISM        unidentified
REFERENCE       1 (bases 1 to 105)
AUTHORS         Quint, W. and Doorn, L.J.V.
TITLE           Probes, methods and kits for detection and typing of Helicobacter
                pylori nucleic acids in biological samples
JOURNAL         Patent: JP 2001502536-A 132 27-FEB-2001;
                INNOGENETICS NV, DDL BV
COMMENT         OS Unidentified
                PN JP 2001502536-A/132
                PD 27-FEB-2001
                PF 10-OCT-1997 JP 1998518004
                PR 16-OCT-1996 EP 96870131.8
                PI WILHELMUS QUINT, LEENDERT JAN VAN DOORN
                PC C12Q1/68, C07K14/205, C12N15/11
                CC
                PH
                FT source Location/Qualifiers
                FT 1. .105 /organism='Unidentified'.
FEATURES       source
                1. .105
                /organism='unidentified'
                /mol_type='genomic DNA'
                /db_xref='taxon:32644'
                21 a 23 g 33 t
BASE COUNT     21 a 23 g 33 t
ORIGIN
Query Match    97.0%; Score 101.8; DB 6; Length 105;
Best Local Similarity 98.1%; Pred. No. 3.5e-22;
Matches 103; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
1 CCCTTTAGTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
|||||
1 CCCTTTAGTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
|||||
61 TCGTCGCTCTTTTACAAACCGTGATCATTCAGCCATTGTTGGGG 105
|||||
61 TCGTCGCTCTTTTACAAACCGTGATCATTCAGCCATTGTTGGGG 105
|||||

RESULT 10
LOCUS          AB057113
DEFINITION     Helicobacter pylori vacA gene for vacuolating cytotoxin, partial
                cds, signal sequence, strain:JapanK26.
ACCESSION      AB057113
VERSION        AB057113.1
KEYWORDS       GI:19910457
SOURCE         Helicobacter pylori
ORGANISM       Helicobacter pylori
REFERENCE       1
AUTHORS        Yamaoka, Y., Gutierrez, O., Saitou, N., Kodama, T., Kim, J.G.,
                Kaishima, K., Ramirez, F.C., Mahachai, V., Osato, M.S. and Graham, D.Y.
TITLE          Helicobacter pylori in North and South America before Columbus:
                Studies of human migration
JOURNAL        Unpublished
REFERENCE       2 (bases 1 to 223)
AUTHORS        Yamaoka, Y., Gutierrez, O., Saitou, N., Kodama, T., Kim, J.G.,
                Kaishima, K., Ramirez, F.C., Mahachai, V., Osato, M.S. and Graham, D.Y.
TITLE          Direct Submission
                Submitted (09-MAR-2001) Yoshio Yamaoka, Baylor College of Medicine,
                Department of Medicine, VA Medical Center (111D), 2002 Holcombe
                Blvd, Houston, Texas 77030, USA (E-mail:yoshio@wt.net,
                Tel:713-790-7234, Fax:713-790-1040)
                Location/Qualifiers
FEATURES       source
                1. .223
                /organism='Helicobacter pylori'
                /mol_type='genomic DNA'
                /strain='JapanO552'
                /db_xref='taxon:210'
                /country='Japan'
                1. .223
                /gene='vacA'
                <1. .>223
                /gene='vacA'
                /note='type slc vacA signal sequence'
                /codon_start=2
                /transl_table=11
                /product='vacuolating cytotoxin'
                /protein_id='BAB87480.1'
                /db_xref='GI:19910458'
                /translation='PLVSLALVGLVLSITPKSHAAFTTIVIPAIVGIGIATGAAGVT
                VSGLLGWLKQAEANKTPDKPKVRIQA'
                55 a 55 c 55 g 58 t
BASE COUNT     55 a 55 c 55 g 58 t
ORIGIN
Query Match    97.0%; Score 101.8; DB 1; Length 223;
Best Local Similarity 98.1%; Pred. No. 3.2e-22;
Matches 103; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
1 CCCTTTAGTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
|||||
1 CCCTTTAGTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
|||||
61 TCGTCGCTCTTTTACAAACCGTGATCATTCAGCCATTGTTGGGG 105
|||||
61 TCGTCGCTCTTTTACAAACCGTGATCATTCAGCCATTGTTGGGG 105
|||||

RESULT 11
LOCUS          AB057141
DEFINITION     Helicobacter pylori vacA gene for vacuolating cytotoxin, partial
                cds, signal sequence, strain:JapanO552.
ACCESSION      AB057141
VERSION        AB057141.1
KEYWORDS       GI:19910513
SOURCE         Helicobacter pylori
ORGANISM       Helicobacter pylori
REFERENCE       1
AUTHORS        Yamaoka, Y., Gutierrez, O., Saitou, N., Kodama, T., Kim, J.G.,
                Kaishima, K., Ramirez, F.C., Mahachai, V., Osato, M.S. and Graham, D.Y.
TITLE          Helicobacter pylori in North and South America before Columbus:
                Studies of human migration
JOURNAL        Unpublished
REFERENCE       2 (bases 1 to 223)
AUTHORS        Yamaoka, Y., Gutierrez, O., Saitou, N., Kodama, T., Kim, J.G.,
                Kaishima, K., Ramirez, F.C., Mahachai, V., Osato, M.S. and Graham, D.Y.
TITLE          Direct Submission
                Submitted (09-MAR-2001) Yoshio Yamaoka, Baylor College of Medicine,
                Department of Medicine, VA Medical Center (111D), 2002 Holcombe
                Blvd, Houston, Texas 77030, USA (E-mail:yoshio@wt.net,
                Tel:713-790-7234, Fax:713-790-1040)
                Location/Qualifiers
FEATURES       source
                1. .223
                /organism='Helicobacter pylori'
                /mol_type='genomic DNA'
                /strain='JapanO552'
                /db_xref='taxon:210'
                /country='Japan'
                1. .223
                /gene='vacA'
                <1. .>223
                /gene='vacA'
                /note='type slc vacA signal sequence'
                /codon_start=2
                /transl_table=11
                /product='vacuolating cytotoxin'

```

/protein_id="BAB87508.1"
/db_xref="GI:19910514"
/translation="PLVSLALVGLVLSITPKSHAAFFTTVIIPALVGGIATGAAGTCA 60
VSGLLGLKQAEANKTPDKPKVWRIQ"
BASE COUNT 57 a 53 c 54 g 59 t
ORIGIN

Query Match 97.0%; Score 101.8; DB 1; Length 223;
Best Local Similarity 98.1%; Pred. No. 3.2e-22;
Matches 103; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
|||||
Db 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
|||||
Qy 61 TGCTGCCCTTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105
|||||
Db 61 TGCTGCCCTTCTTTACACCGTGATCATTCAGCCATTGTTGGAGG 105
|||||

RESULT 12
AB057158 223 bp DNA linear BCT 02-APR-2002
LOCUS
DEFINITION Helicobacter pylori vacA gene for vacuolating cytotoxin, partial
cde, signal sequence, strain:Vietnam2692.
ACCESSION AB057158
VERSION AB057158.1 GI:19910547
KEYWORDS
SOURCE Helicobacter pylori
ORGANISM Helicobacter pylori
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
Helicobacteraceae; Helicobacter.

REFERENCE 1
AUTHORS Yamaoka,Y., Gutierrez,O., Saitou,N., Kodama,T., Kim,J.G.,
Kashima,K., Ramirez,F.C., Mahachai,V., Osato,M.S. and Graham,D.Y.
TITLE Helicobacter pylori in North and South America before Columbus:
Studies of human migration
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 223)
AUTHORS Yamaoka,Y., Gutierrez,O., Saitou,N., Kodama,T., Kim,J.G.,
Kashima,K., Ramirez,F.C., Mahachai,V., Osato,M.S. and Graham,D.Y.
TITLE Direct Submission
JOURNAL Submitted (09-MAR-2001) Yoshio Yamaoka, Baylor College of Medicine,
Department of Medicine, VA Medical Center (111D), 2002 Holcombe
Blvd, Houston, Texas 77030, USA (E-mail:yoshio@wt.net,
Tel:713-790-7234, Fax:713-790-1040)
FEATURES
source
1..223
/organism="Helicobacter pylori"
/mol_type="genomic DNA"
/strain="Vietnam2692"
/db_xref="taxon:210"
/country="Viet Nam"
1..223
/genes="vacA"
<1..>223
/genes="vacA"
/notes="type alc vacA signal sequence"
/codon_start=2
/transl_table=11
/product="vacuolating cytotoxin"
/protein_id="BAB87525.1"
/db_xref="GI:19910548"
/translations="PLVSLALVGLVLSITPKSHAAFFTTVIIPALVGGIATGAAGTCA 60
VSGLLGLKQAEANKTPDKPKVWRIQ"
BASE COUNT 56 a 54 c 55 g 58 t
ORIGIN

Query Match 97.0%; Score 101.8; DB 1; Length 223;
Best Local Similarity 98.1%; Pred. No. 3.2e-22;
Matches 103; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
|||||
Db 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
|||||
Qy 61 TGCTGCCCTTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105
|||||
Db 61 TGCTGCCCTTCTTTACACCGTGATCATTCAGCCATTGTTGGAGG 105
|||||

RESULT 12
AB057158 223 bp DNA linear BCT 02-APR-2002
LOCUS
DEFINITION Helicobacter pylori vacA gene for vacuolating cytotoxin, partial
cde, signal sequence, strain:Vietnam2692.
ACCESSION AB057158
VERSION AB057158.1 GI:19910547
KEYWORDS
SOURCE Helicobacter pylori
ORGANISM Helicobacter pylori
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
Helicobacteraceae; Helicobacter.

REFERENCE 1
AUTHORS Yamaoka,Y., Gutierrez,O., Saitou,N., Kodama,T., Kim,J.G.,
Kashima,K., Ramirez,F.C., Mahachai,V., Osato,M.S. and Graham,D.Y.
TITLE Helicobacter pylori in North and South America before Columbus:
Studies of human migration
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 223)
AUTHORS Yamaoka,Y., Gutierrez,O., Saitou,N., Kodama,T., Kim,J.G.,
Kashima,K., Ramirez,F.C., Mahachai,V., Osato,M.S. and Graham,D.Y.
TITLE Direct Submission
JOURNAL Submitted (09-MAR-2001) Yoshio Yamaoka, Baylor College of Medicine,
Department of Medicine, VA Medical Center (111D), 2002 Holcombe
Blvd, Houston, Texas 77030, USA (E-mail:yoshio@wt.net,
Tel:713-790-7234, Fax:713-790-1040)
FEATURES
source
1..223
/organism="Helicobacter pylori"
/mol_type="genomic DNA"
/strain="Vietnam2692"
/db_xref="taxon:210"
/country="Viet Nam"
1..223
/genes="vacA"
<1..>223
/genes="vacA"
/notes="type alc vacA signal sequence"
/codon_start=2
/transl_table=11
/product="vacuolating cytotoxin"
/protein_id="BAB87525.1"
/db_xref="GI:19910548"
/translations="PLVSLALVGLVLSITPKSHAAFFTTVIIPALVGGIATGAAGTCA 60
VSGLLGLKQAEANKTPDKPKVWRIQ"
BASE COUNT 56 a 54 c 55 g 58 t
ORIGIN

Db 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
|||||
Qy 61 TGCTGCCCTTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105
|||||
Db 61 TGCTGCCCTTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105
|||||

RESULT 13
AF050377 256 bp DNA linear BCT 20-JAN-2000
LOCUS
DEFINITION Helicobacter pylori isolate CHN4952ass vacuolating cytotoxin
precursor (vacA) gene, partial cds.
ACCESSION AF050377
VERSION AF050377.1 GI:6716247
KEYWORDS
SOURCE Helicobacter pylori
ORGANISM Helicobacter pylori
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
Helicobacteraceae; Helicobacter.

REFERENCE 1 (bases 1 to 256)
AUTHORS Ji,X., Telford,J.L., Burroni,D., Guidotti,S., Pagliaccia,C.,
Rayrat,J.M., Xu,G. and Rappuoli,R.
TITLE Allelic variation of vacA gene in the Chinese Helicobacter pylori
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 256)
AUTHORS Ji,X., Telford,J.L., Burroni,D., Guidotti,S., Pagliaccia,C.,
Rayrat,J.M. and Rappuoli,R.
TITLE Direct Submission
JOURNAL Submitted (25-FEB-1998) Molecular Biology of IRIS, Chiron Vaccines,
via Fiorentina 1, Siena 53100, Italy
FEATURES
source
1..256
/organism="Helicobacter pylori"
/mol_type="genomic DNA"
/strain="CHN4952a"
/isolate="CHN4952ass"
/db_xref="taxon:210"
1..>256
/genes="vacA"
1..>256
/genes="vacA"
/codon_start=1
/transl_table=11
/product="vacuolating cytotoxin precursor"
/protein_id="AAP26559.1"
/db_xref="GI:6716248"
/translation="MELOQTHRKINRPLVSLALVGLVLSITPKSHAAFFTTVIIPAI
VGGIAGGAAGTGVSGLLGWLKQAEANKTPDKPKVWRIQ"
BASE COUNT 69 a 63 c 61 g 63 t
ORIGIN

Query Match 97.0%; Score 101.8; DB 1; Length 256;
Best Local Similarity 98.1%; Pred. No. 3.1e-22;
Matches 103; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
|||||
Db 36 CCCTTTAGTTTCTCTCGCTTTAGTGGGGTTATTGGTCAGCATCACACCGCAAAAAAGTCA 95
|||||
Qy 61 TGCTGCCCTTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105
|||||
Db 96 TGCCGCCCTTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 140
|||||

RESULT 14
AF091830 631 bp DNA linear BCT 10-DEC-2001
LOCUS
DEFINITION Helicobacter pylori T-34 vacuolating cytotoxin precursor (vacA)
gene, partial cds.
ACCESSION AF091830
VERSION AF091830.1 GI:4566467
KEYWORDS

SOURCE Helicobacter pylori
ORGANISM Helicobacter pylori
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
Helicobacteraceae; Helicobacter.

REFERENCE 1 (bases 1 to 631)
AUTHORS Lin, C.W., Wu, S.C., Lee, S.C. and Cheng, K.S.
TITLE Genetic analysis and clinical evaluation of vacuolating cytotoxin gene A and cytotoxin-associated gene A in Taiwanese Helicobacter pylori isolates from peptic ulcer patients
JOURNAL Scand. J. Infect. Dis. 32 (1), 51-57 (2000)
MEDLINE 20178822
PUBMED 10716078

REFERENCE 2 (bases 1 to 631)
AUTHORS Lin, C.W.
TITLE Direct Submission
JOURNAL Submitted (10-SEP-1998) School of Medical Technology, China Medical College, Taichung, Taiwan 404, Republic of China

FEATURES
source
1..631
/organism="Helicobacter pylori"
/mol_type="genomic DNA"
/isolates="T-34"
/db_xref="taxon:210"
/country="Taiwan"
1..>631
/genes="vaca"
1..>631
/gene="vaca"
/note="N-terminal region"
/codon_start=1
/transl_table=11
/product="vacuolating cytotoxin precursor"
/protein_id="AA023367.1"
/db_xref="GI:4566468"
VGIASGAAVGVTVGLGLGKLAQAEANKTPDKPKWFIQAGRFNFPNKEYLDYK
SLLSKIDGWMGNARHYWYKGGWNKLEVDMDAIGTYKLGLRNTTGGDLVNM
QKATRLGQFNSTSFKDSADRTVRVDFNAKNISIDNFIENNRVGGG"
BASE COUNT 189 a 123 c 153 g 166 t
ORIGIN

Query Match 97.0%; Score 101.8; DB 1; Length 631;
Best Local Similarity 98.1%; Pred. No. 2.8e-22; Indels 0; Gaps 0;
Matches 103; Conservative 0; Mismatches 2;

Y 1 CCCTTAGTTCTCTCGCTTAGTGGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
|||
b 36 CCCTTAGTTCTCTCGCTTAGTGGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 95
|||
Y 61 TGCTGCTTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105
|||
b 96 TGCCGCTTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 140
|||

RESULT 15
PY390723
OCUS Helicobacter pylori partial vaca gene for vacA protein, isolate
EFINITION HP390723 105 bp DNA linear BCT 22-DEC-1999
NZ9524.

CCESSION AJ390723
ERSION AJ390723.1 GI:6634392
EYWORDS vacA gene; vacA protein.
SOURCE Helicobacter pylori
ORGANISM Helicobacter pylori
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
Helicobacteraceae; Helicobacter.

REFERENCE 1
AUTHORS van Doorn, L.J., Figueiredo, C., Sama, R., Pena, S., Midolo, P.,
Ng, E.K., Atherton, J.C., Blaser, M.J. and Quint, W.G.
TITLE Expanding allelic diversity of Helicobacter pylori vacA
JOURNAL J. Clin. Microbiol. 36 (9), 2597-2603 (1998)
MEDLINE 98371059
PUBMED 9705399

REFERENCE 2 (bases 1 to 105)
AUTHORS van Doorn, L.J.
TITLE Direct Submission
JOURNAL Submitted (21-OCT-1999) van Doorn L.J., Molecular Biology, Delft
Diagnostic Laboratory, R. de Graafweg 7, Delft, 2625 AD,
NETHERLANDS

FEATURES
source
1..105
/organism="Helicobacter pylori"
/mol_type="genomic DNA"
/isolates="N29524"
/db_xref="taxon:210"
/country="New Zealand"
1..105
/genes="vaca"
<1..>105
/gene="vaca"
/function="cytotoxin"
/note="s-region"
/codon_start=2
/transl_table=11
/product="vacA protein"
/protein_id="CA864434.1"
/db_xref="GI:6634393"
/translation="ELVSLALVGLLVISITPQKSHAAFTTVIIPAIVGG"
BASE COUNT 20 a 28 c 24 g 33 t
ORIGIN

Query Match 95.4%; Score 100.2; DB 1; Length 105;
Best Local Similarity 97.1%; Pred. No. 1.2e-21; Indels 0; Gaps 0;
Matches 102; Conservative 0; Mismatches 3;

QY 1 CCCTTAGTTCTCTCGCTTAGTGGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
|||
Db 1 CCCTTAGTTCTCTCGCTTAGTGGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
|||
QY 61 TGCTGCTTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105
|||
Db 61 TGCCGCTTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105
|||

Search completed: January 13, 2004, 02:12:05
Job time : 2661 secs

1	105	100.0	105	19	AAV73634	H. pylori	vaca	S-r
2	105	100.0	105	19	AAV73635	H. pylori	vaca	S-r
3	103.4	98.5	105	19	AAV73636	H. pylori	vaca	S-r
4	101.8	97.0	105	19	AAV73640	H. pylori	vaca	S-r
5	100.2	95.4	105	19	AAV73637	H. pylori	vaca	S-r
6	100.2	95.4	105	19	AAV73639	H. pylori	vaca	S-r
7	100.2	95.4	105	19	AAV73641	H. pylori	vaca	S-r
8	99.4	94.7	105	19	AAV73638	H. pylori	vaca	S-r

PI Quint W, Van Doorn L;

KW PCR primer; probe; vacA; cagA; detection; vacuolating toxin; VDG:

PI Quint W, Van Doorn L;

```

XX WPI; 1998-251300/22.
XX
XX Method for detecting and/or typing Helicobacter pylori strains -
PT comprises use of primers and probes based on vacA and cagA gene
XX
XX Claim 19; Figure 12; 122pp; English.
XX
XX This invention describes a novel method for the detection and/or typing
CC of Helicobacter pylori strains present in a sample using PCR primers and
CC probes to detect regions of the vacuolating toxin (vacA) gene and other
CC virulence determinant genes (VDG) e.g. the cytotoxin-associated (cagA)
CC gene. The method allows the typing and allele-specific detection of a
CC strain according to the VDG alleles present in that particular H. pylori
CC strain. The virulence determinant genes are the genetic elements
CC involved in enabling, determining, and marking the infectivity and/or
CC pathogenicity of the H. pylori strain. The method provides a way of
CC detecting H. pylori strains in a sample with respect to the development
CC of chronic active gastritis, gastric and duodenal ulcers, gastric
CC adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or
CC determining eradication therapy. AAV73508-V73546 represent PCR primers
CC and probes used in the detection of the H. pylori vacA and cagA genes.
CC The primers and probes are used especially to detect the vacA S regions
CC S1a/b/c and S2 and the M regions M1 and M2 which are represented in
CC AAV73547-V73785.
XX
XX Sequence 105 BP; 22 A; 27 C; 22 G; 34 T; 0 other;
SQ
Query Match 100.0%; Score 105; DB 19; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.1e-25;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAGTCA 60
DB 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAGTCA 60

QY 61 TGTGCTCTCTTTACACCGTGATCATTCAGCCATTGTGGGG 105
DB 61 TGTGCTCTCTTTACACCGTGATCATTCAGCCATTGTGGGG 105

RESULT 2
AAV73635
ID AAV73635 standard; DNA; 105 BP.
AC AAV73635;
XX
XX 22-MAR-2000 (first entry)
DT
DE H. pylori vacA S-region s1c DNA fragment N3001.
XX
XX PCR primer; probe; vacA; cagA; detection; vacuolating toxin; VDG;
XX virulence determinant gene; cytotoxin-associated gene; allele-specific;
XX infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer;
XX adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy;
XX S region; S1a; S1b; S1c; S2; M region; M1; M2; ss.
XX
XX Helicobacter pylori.
XX
XX WO9816658-A2.
XX
XX 23-APR-1998.
XX
XX 10-OCT-1997; 97WO-EP05614.
XX
XX 16-OCT-1996; 96EP-0870131.
XX
XX 09-SEP-1997; 97EP-0870133.
XX
XX (INNO-) INNOGENETICS NV.
XX (DDL-) DDL BV.
XX
XX Quint W, Van Doorn L;
XX
XX WPI; 1998-251300/22.

```

XX Method for detecting and/or typing *Helicobacter pylori* strains -
 PT comprises use of primers and probes based on vacA and caga gene
 XX Claim 19; Figure 12; 122pp; English.
 XX This invention describes a novel method for the detection and/or typing
 CC of *Helicobacter pylori* strains present in a sample using PCR primers and
 CC probes to detect regions of the vacuolating toxin (vacA) gene and other
 CC virulence determinant genes (VDG) e.g. the cytotoxin-associated (caga)
 CC gene. The method allows the typing and allele-specific detection of a
 CC strain according to the VDG alleles present in that particular *H. pylori*
 CC strain. The virulence determinant genes are the genetic elements
 CC involved in enabling, determining, and marking the infectivity and/or
 CC pathogenicity of the *H. pylori* strain. The method provides a way of
 CC detecting *H. pylori* strains in a sample with respect to the development
 CC of chronic active gastritis, gastric and duodenal ulcers, gastric
 CC adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or
 CC determining eradication therapy. AAV73508-V73546 represent PCR primers
 CC and probes used in the detection of the *H. pylori* vacA and caga genes.
 CC The primers and probes are used especially to detect the vacA S regions
 CC S1a/b/c and S2 and the M regions M1 and M2 which are represented in
 CC AAV73547-V73785.
 XX Sequence 105 BP; 21 A; 27 C; 23 G; 34 T; 0 other;
 SQ

Query Match 98.5%; Score 103.4; DB 19; Length 105;
 Best Local Similarity 99.0%; Pred. No. 1.4e-24;
 Matches 104; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 CCCTTTAGTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
 1 CCCTTTAGTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCGCAAAAAAGTCA 60

61 TGCTGCTCTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105
 61 TGCTGCTCTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105

RESULT 4
 AAV73640
 ID AAV73640 standard; DNA; 105 BP.
 XX AC AAV73640;
 XX 22-MAR-2000 (first entry)
 XX H. pylori vacA S-region s1c DNA fragment TH8B35001.
 XX PCR primer; probe; vacA; caga; detection; vacuolating toxin; VDG;
 XX virulence determinant gene; cytotoxin-associated gene; allele-specific;
 XX infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer;
 XX adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy;
 XX S region; S1a; S1b; S1c; S2; M region; M1; M2; ss.
 XX *Helicobacter pylori*.
 XX WO9816658-A2.
 XX 23-APR-1998.
 XX 10-OCT-1997; 97WO-EP05614.
 XX 16-OCT-1996; 96EP-0870131.
 XX 09-SEP-1997; 97EP-0870133.
 XX (INNO-3) INNOGENETICS NV.
 XX COLLEGE BDL BV.
 XX Quint W. Van Doorn L;
 XX WPI; 1998-251300/22.
 XX Method for detecting and/or typing *Helicobacter pylori* strains -

PT Method for detecting and/or typing *Helicobacter pylori* strains -
 PT comprises use of primers and probes based on vacA and caga gene
 XX Claim 19; Figure 12; 122pp; English.
 XX This invention describes a novel method for the detection and/or typing
 CC of *Helicobacter pylori* strains present in a sample using PCR primers and
 CC probes to detect regions of the vacuolating toxin (vacA) gene and other
 CC virulence determinant genes (VDG) e.g. the cytotoxin-associated (caga)
 CC gene. The method allows the typing and allele-specific detection of a
 CC strain according to the VDG alleles present in that particular *H. pylori*
 CC strain. The virulence determinant genes are the genetic elements
 CC involved in enabling, determining, and marking the infectivity and/or
 CC pathogenicity of the *H. pylori* strain. The method provides a way of
 CC detecting *H. pylori* strains in a sample with respect to the development
 CC of chronic active gastritis, gastric and duodenal ulcers, gastric
 CC adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or
 CC determining eradication therapy. AAV73508-V73546 represent PCR primers
 CC and probes used in the detection of the *H. pylori* vacA and caga genes.
 CC The primers and probes are used especially to detect the vacA S regions
 CC S1a/b/c and S2 and the M regions M1 and M2 which are represented in
 CC AAV73547-V73785.
 XX Sequence 105 BP; 21 A; 28 C; 23 G; 33 T; 0 other;
 SQ

Query Match 97.0%; Score 101.8; DB 19; Length 105;
 Best Local Similarity 98.1%; Pred. No. 4.7e-24;
 Matches 103; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 CCCTTTAGTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
 1 CCCTTTAGTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCGCAAAAAAGTCA 60

61 TGCTGCTCTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105
 61 TGCTGCTCTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105

RESULT 5
 AAV73637
 ID AAV73637 standard; DNA; 105 BP.
 XX AC AAV73637;
 XX 22-MAR-2000 (first entry)
 XX H. pylori vacA S-region s1c DNA fragment HK41001.
 XX PCR primer; probe; vacA; caga; detection; vacuolating toxin; VDG;
 XX virulence determinant gene; cytotoxin-associated gene; allele-specific;
 XX infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer;
 XX adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy;
 XX S region; S1a; S1b; S1c; S2; M region; M1; M2; ss.
 XX *Helicobacter pylori*.
 XX WO9816658-A2.
 XX 23-APR-1998.
 XX 10-OCT-1997; 97WO-EP05614.
 XX 16-OCT-1996; 96EP-0870131.
 XX 09-SEP-1997; 97EP-0870133.
 XX (INNO-3) INNOGENETICS NV.
 XX COLLEGE BDL BV.
 XX Quint W. Van Doorn L;
 XX WPI; 1998-251300/22.
 XX Method for detecting and/or typing *Helicobacter pylori* strains -

PT comprises use of primers and probes based on vacA and cagA gene

XX Claim 19; Figure 12; 122pp; English.

XX This invention describes a novel method for the detection and/or typing
XX of Helicobacter pylori strains present in a sample using PCR primers and
XX probes to detect regions of the vacuolating toxin (vacA) gene and other
XX virulence determinant genes (VDG) e.g. the cytotoxin-associated (cagA)
XX gene. The method allows the typing and allele-specific detection of a
XX strain according to the VDG alleles present in that particular H. pylori
XX strain. The virulence determinant genes are the genetic elements
XX involved in enabling, determining, and marking the infectivity and/or
XX pathogenicity of the H. pylori strain. The method provides a way of
XX detecting H. pylori strains in a sample with respect to the development
XX of chronic active gastritis, gastric and duodenal ulcers, gastric
XX adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or
XX determining eradication therapy. AAV73508-V73546 represent PCR primers
XX and probes used in the detection of the H. pylori vacA and cagA genes.
XX The primers and probes are used especially to detect the vacA S regions
XX S1a/b/c and S2 and the M regions M1 and M2 which are represented in
XX AAV73547-V73785.

SQ Sequence 105 BP; 21 A; 29 C; 23 G; 32 T; 0 other;

Query Match 95.4%; Score 100.2; DB 19; Length 105;
Best Local Similarity 97.1%; Pred. No. 1.6e-23;
Matches 102; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
DB 1 CCCTCTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCGCAAAAAAGTCA 60

QY 61 TGCTGCTCTCTTTACACCGTGATCATTCAGCCATTGTGGGG 105
DB 61 TGGCGCTCTTTACACCGTGATCATTCAGCCATTGTGGGG 105

RESULT 6

AAV73639

ID AAV73639 standard; DNA; 105 BP.

XX AAV73639;

XX 22-MAR-2000 (first entry)

DE H. pylori vacA S-region s1c DNA fragment 95_24001.

XX PCR primer; probe; vacA; cagA; detection; vacuolating toxin; VDG;
KW virulence determinant gene; cytotoxin-associated gene; allele-specific;
KW infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer;
KW adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy;
KW S region; S1a; S1b; S1c; S2; M region; M1; M2; ss.

XX Helicobacter pylori.

XX WO9816658-A2.

XX 23-APR-1998.

XX 10-OCT-1997; 97WO-EP05614.

XX 16-OCT-1996; 96EP-0870131.

XX 09-SEP-1997; 97EP-0870133.

XX (INNO-) INNOGENETICS NV.

XX (DDL-) DDL BV.

XX Quint W, Van Doorn L;

XX WPI; 1998-251300/22.

XX Method for detecting and/or typing Helicobacter pylori strains -
PT comprises use of primers and probes based on vacA and cagA gene

XX Claim 19; Figure 12; 122pp; English.

XX This invention describes a novel method for the detection and/or typing
XX of Helicobacter pylori strains present in a sample using PCR primers and
XX probes to detect regions of the vacuolating toxin (vacA) gene and other
XX virulence determinant genes (VDG) e.g. the cytotoxin-associated (cagA)
XX gene. The method allows the typing and allele-specific detection of a
XX strain according to the VDG alleles present in that particular H. pylori
XX strain. The virulence determinant genes are the genetic elements
XX involved in enabling, determining, and marking the infectivity and/or
XX pathogenicity of the H. pylori strain. The method provides a way of
XX detecting H. pylori strains in a sample with respect to the development
XX of chronic active gastritis, gastric and duodenal ulcers, gastric
XX adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or
XX determining eradication therapy. AAV73508-V73546 represent PCR primers
XX and probes used in the detection of the H. pylori vacA and cagA genes.
XX The primers and probes are used especially to detect the vacA S regions
XX S1a/b/c and S2 and the M regions M1 and M2 which are represented in
XX AAV73547-V73785.

SQ Sequence 105 BP; 20 A; 28 C; 24 G; 33 T; 0 other;

Query Match 95.4%; Score 100.2; DB 19; Length 105;
Best Local Similarity 97.1%; Pred. No. 1.6e-23;
Matches 102; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
DB 1 CCCTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCGCAAAAAAGTCA 60

QY 61 TGCTGCTCTCTTTACACCGTGATCATTCAGCCATTGTGGGG 105

DB 61 TGGCGCTCTTTACACCGTGATCATTCAGCCATTGTGGGG 105

RESULT 7

AAV73641

ID AAV73641 standard; DNA; 105 BP.

XX AAV73641;

XX 22-MAR-2000 (first entry)

DE H. pylori vacA S-region s1c DNA fragment TH8828001.

XX PCR primer; probe; vacA; cagA; detection; vacuolating toxin; VDG;
KW virulence determinant gene; cytotoxin-associated gene; allele-specific;
KW infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer;
KW adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy;
KW S region; S1a; S1b; S1c; S2; M region; M1; M2; ss.

XX Helicobacter pylori.

XX WO9816658-A2.

XX 23-APR-1998.

XX 10-OCT-1997; 97WO-EP05614.

XX 16-OCT-1996; 96EP-0870131.

XX 09-SEP-1997; 97EP-0870133.

XX (INNO-) INNOGENETICS NV.

XX (DDL-) DDL BV.

XX Quint W, Van Doorn L;

XX WPI; 1998-251300/22.

XX Method for detecting and/or typing Helicobacter pylori strains -
PT comprises use of primers and probes based on vacA and cagA gene

Claim 19; Figure 12; 122pp; English.

This invention describes a novel method for the detection and/or typing of *Helicobacter pylori* strains present in a sample using PCR primers and probes to detect regions of the vacuolating toxin (vaca) gene and other virulence determinant genes (VDG) e.g. the cytotoxin-associated (caga) gene. The method allows the typing and allele-specific detection of a strain according to the VDG alleles present in that particular *H. pylori* strain. The virulence determinant genes are the genetic elements involved in enabling, determining, and marking the infectivity and/or pathogenicity of the *H. pylori* strain. The method provides a way of detecting *H. pylori* strains in a sample with respect to the development of chronic active gastritis, gastric and duodenal ulcers, gastric adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or determining eradication therapy. AAV73508-V73546 represent PCR primers and probes used in the detection of the *H. pylori* vaca and caga genes. The primers and probes are used especially to detect the vaca S regions S1a/b/c and S2 and the M regions M1 and M2 which are represented in AAV73547-V73785.

Sequence 105 BP; 21 A; 29 C; 23 G; 32 T; 0 other;

Query Match 95.4%; Score 100.2; DB 19; Length 105;
Best Local Similarity 97.1%; Pred. No. 1.6e-23;
Matches 102; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
1 CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCGCAAAAAAGTCA 60

61 TGCTGCCCTTCTTTACAACCGTGATCATTCAGCCATTGTTGGGGG 105
61 TGCCGCTTCTTTACAACCGTGATCATTCAGCCATTGTTGGGGG 105

RESULT 8
AAV73638
ID AAV73638 standard; DNA; 105 BP.

AAV73638;

22-MAR-2000 (first entry)

H. pylori vaca S-region s1c DNA fragment HK35001.

PCR primer; probe; vaca; caga; detection; vacuolating toxin; VDG; virulence determinant gene; cytotoxin-associated gene; allele-specific; infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer; adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy; S region; S1a; S1b; S1c; S2; M region; M1; M2; ss.

Helicobacter pylori.

WO9816658-A2.

23-APR-1998.

10-OCT-1997; 97WO-EP05614.

16-OCT-1996; 96EP-0870131.

09-SEP-1997; 97EP-0870133.

(INNO-) INNOGENETICS NV.

(DDL-) DDL BV.

Quint W, Van Doorn L;

WPI; 1998-251300/22.

Method for detecting and/or typing *Helicobacter pylori* strains - comprises use of primers and probes based on vaca and caga gene

Claim 19; Figure 12; 122pp; English.

XX

This invention describes a novel method for the detection and/or typing of *Helicobacter pylori* strains present in a sample using PCR primers and probes to detect regions of the vacuolating toxin (vaca) gene and other virulence determinant genes (VDG) e.g. the cytotoxin-associated (caga) gene. The method allows the typing and allele-specific detection of a strain according to the VDG alleles present in that particular *H. pylori* strain. The virulence determinant genes are the genetic elements involved in enabling, determining, and marking the infectivity and/or pathogenicity of the *H. pylori* strain. The method provides a way of detecting *H. pylori* strains in a sample with respect to the development of chronic active gastritis, gastric and duodenal ulcers, gastric adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or determining eradication therapy. AAV73508-V73546 represent PCR primers and probes used in the detection of the *H. pylori* vaca and caga genes. The primers and probes are used especially to detect the vaca S regions S1a/b/c and S2 and the M regions M1 and M2 which are represented in AAV73547-V73785.

Sequence 105 BP; 21 A; 29 C; 22 G; 32 T; 1 other;

Query Match 94.7%; Score 99.4; DB 19; Length 105;
Best Local Similarity 96.2%; Pred. No. 2.9e-23;
Matches 101; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

1 CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
1 CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCGCAAAAAAGTCA 60

61 TGCTGCCCTTCTTTACAACCGTGATCATTCAGCCATTGTTGGGGG 105
61 TGCCGCTTCTTTACAACCGTGATCATTCAGCCATTGTTGGGGG 105

RESULT 9

AAV73644

ID AAV73644 standard; DNA; 105 BP.

AAV73644;

22-MAR-2000 (first entry)

H. pylori vaca S-region s1c DNA fragment HK46001.

PCR primer; probe; vaca; caga; detection; vacuolating toxin; VDG; virulence determinant gene; cytotoxin-associated gene; allele-specific; infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer; adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy; S region; S1a; S1b; S1c; S2; M region; M1; M2; ss.

Helicobacter pylori.

WO9816658-A2.

23-APR-1998.

10-OCT-1997; 97WO-EP05614.

16-OCT-1996; 96EP-0870131.

09-SEP-1997; 97EP-0870133.

(INNO-) INNOGENETICS NV.

(DDL-) DDL BV.

Quint W, Van Doorn L;

WPI; 1998-251300/22.

Method for detecting and/or typing *Helicobacter pylori* strains - comprises use of primers and probes based on vaca and caga gene

Claim 19; Figure 12; 122pp; English.

CC This invention describes a novel method for the detection and/or typing
 CC of Helicobacter pylori strains present in a sample using PCR primers and
 CC probes to detect regions of the vacuolating toxin (vacA) gene and other
 CC virulence determinant genes (VDG) e.g. the cytotoxin-associated (cagA)
 CC gene. The method allows the typing and allele-specific detection of a
 CC strain according to the VDG alleles present in that particular H. pylori
 CC strain. The virulence determinant genes are the genetic elements
 CC involved in enabling, determining, and marking the infectivity and/or
 CC pathogenicity of the H. pylori strain. The method provides a way of
 CC detecting H. pylori strains in a sample with respect to the development
 CC of chronic active gastritis, gastric and duodenal ulcers, gastric
 CC adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or
 CC determining eradication therapy. AAV73508-V73546 represent PCR primers
 CC and probes used in the detection of the H. pylori vacA and cagA genes.
 CC The primers and probes are used especially to detect the vacA S regions
 CC S1a/b/c and S2 and the M regions M1 and M2 which are represented in
 CC AAV73547-V73785.

XX
 SQ Sequence 105 BP; 23 A; 28 C; 21 G; 33 T; 0 other;
 Query Match 93.9%; Score 98.6; DB 19; Length 105;
 Best Local Similarity 96.2%; Pred. No. 5.3e-23;
 Matches 101; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
 Db 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
 QY 61 TGTGCGCTTTTACACCGTGATCATTTCCAGCCATTGTTGGGG 105
 Db 61 TGCCGCGCTTTTACACCGTGATCATTTCCAGCCATTGTTGGAG 105

RESULT 10
 AAV73645
 ID AAV73645 standard; DNA; 105 BP.
 XX
 AC AAV73645;
 XX
 DT 22-MAR-2000 (first entry)
 XX
 DE H. pylori vacA S-region s1c DNA fragment TH8932001.
 XX
 KW PCR primer; probe; vacA; cagA; detection; vacuolating toxin; VDG;
 KW virulence determinant gene; cytotoxin-associated gene; allele-specific;
 KW infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer;
 KW adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy;
 KW S region; S1a; S1b; S1c; S2; M region; M1; M2; ss.
 XX
 OS Helicobacter pylori.
 XX
 PN WO9816658-A2.
 XX
 PD 23-APR-1998.
 XX
 PF 10-OCT-1997; 97WO-EP05614.
 XX
 PR 16-OCT-1996; 96EP-0870131.
 PR 09-SEP-1997; 97EP-0870133.
 XX
 XX (INNO-) INNOGENETICS NV.
 PA (DDLD-) DDL BV.
 XX
 PI Quint W, Van Doorn L;
 XX
 DR WPI, 1998-251300/22.
 XX
 XX Method for detecting and/or typing Helicobacter pylori strains
 PT comprises use of primers and probes based on vacA and cagA gene
 XX
 PS Claim 19; Figure 12; 122pp; English.
 XX
 CC This invention describes a novel method for the detection and/or typing

CC of Helicobacter pylori strains present in a sample using PCR primers and
 CC probes to detect regions of the vacuolating toxin (vacA) gene and other
 CC virulence determinant genes (VDG) e.g. the cytotoxin-associated (cagA)
 CC gene. The method allows the typing and allele-specific detection of a
 CC strain according to the VDG alleles present in that particular H. pylori
 CC strain. The virulence determinant genes are the genetic elements
 CC involved in enabling, determining, and marking the infectivity and/or
 CC pathogenicity of the H. pylori strain. The method provides a way of
 CC detecting H. pylori strains in a sample with respect to the development
 CC of chronic active gastritis, gastric and duodenal ulcers, gastric
 CC adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or
 CC determining eradication therapy. AAV73508-V73546 represent PCR primers
 CC and probes used in the detection of the H. pylori vacA and cagA genes.
 CC The primers and probes are used especially to detect the vacA S regions
 CC S1a/b/c and S2 and the M regions M1 and M2 which are represented in
 CC AAV73547-V73785.

XX
 SQ Sequence 105 BP; 23 A; 28 C; 21 G; 33 T; 0 other;
 Query Match 93.9%; Score 98.6; DB 19; Length 105;
 Best Local Similarity 96.2%; Pred. No. 5.3e-23;
 Matches 101; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
 Db 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
 QY 61 TGTGCGCTTTTACACCGTGATCATTTCCAGCCATTGTTGGGG 105
 Db 61 TGCCGCGCTTTTACACCGTGATCATTTCCAGCCATTGTTGGAG 105

RESULT 11
 AAV73550
 ID AAV73550 standard; DNA; 176 BP.
 XX
 AC AAV73550;
 XX
 DT 22-MAR-2000 (first entry)
 XX
 DE H. pylori S-region S1a/b fragment C4082_Va1F.
 XX
 KW PCR primer; probe; vacA; cagA; detection; vacuolating toxin; VDG;
 KW virulence determinant gene; cytotoxin-associated gene; allele-specific;
 KW infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer;
 KW adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy;
 KW S region; S1a; S1b; S1c; S2; M region; M1; M2; ss.
 XX
 OS Helicobacter pylori.
 XX
 PN WO9816658-A2.
 XX
 PD 23-APR-1998.
 XX
 PF 10-OCT-1997; 97WO-EP05614.
 XX
 PR 16-OCT-1996; 96EP-0870131.
 PR 09-SEP-1997; 97EP-0870133.
 XX
 XX (INNO-) INNOGENETICS NV.
 PA (DDLD-) DDL BV.
 XX
 PI Quint W, Van Doorn L;
 XX
 DR WPI, 1998-251300/22.
 XX
 XX Method for detecting and/or typing Helicobacter pylori strains
 PT comprises use of primers and probes based on vacA and cagA gene
 XX
 PS Claim 17; Figure 2a; 122pp; English.
 XX
 CC This invention describes a novel method for the detection and/or typing
 CC of Helicobacter pylori strains present in a sample using PCR primers and

CC probes to detect regions of the vacuolating toxin (vaca) gene and other
 CC virulence determinant genes (VDG) e.g. the cytotoxin-associated (caga)
 CC gene. The method allows the typing and allele-specific detection of a
 CC strain according to the VDG alleles present in that particular H. pylori
 CC strain. The virulence determinant genes are the genetic elements
 CC involved in enabling, determining, and marking the infectivity and/or
 CC pathogenicity of the H. pylori strain. The method provides a way of
 CC detecting H. pylori strains in a sample with respect to the development
 CC of chronic active gastritis, gastric and duodenal ulcers, gastric
 CC adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or
 CC determining eradication therapy. AAV73508-V73546 represent PCR primers
 CC and probes used in the detection of the H. pylori vacA and caga genes.
 CC The primers and probes are used especially to detect the vacA S regions
 CC S1a/b/c and S2 and the M regions M1 and M2 which are represented in
 CC AAV73547-V73785.

XX Sequence 176 BP; 39 A; 43 C; 45 G; 49 T; 0 other;
 SQ Query Match 93.98; Score 98.6; DB 19; Length 176;
 Best Local Similarity 96.24; Pred. No. 6.1e-23;
 Matches 101; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
 DB 2 CCCTTTAGTTTCTCTCGCTTTAGTGGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 61
 JY 61 TGTGCTCTTTTACAAACCGTGATCATTTCCAGCCATTGTTGGGG 105
 DB 62 TGCGCGCTTTTACAAACCGTGATCATTTCCAGCCATTGTTGGAGG 106

RESULT 12
 AAV73650
 ID AAV73650 standard; DNA; 105 BP.
 AC AAV73650;
 XX AAV73650;
 DT 22-MAR-2000 (first entry)
 DE H. pylori vacA S-region s1c DNA fragment CH4001.

XX PCR primer; probe; vacA; caga; detection; vacuolating toxin; VDG;
 XX virulence determinant gene; cytotoxin-associated gene; allele-specific;
 XX infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer;
 XX adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy;
 XX S region; S1a; S1b; S1c; S2; M region; M1; M2; ss.

XX Helicobacter pylori.
 XX WO9816558-A2.
 XX 23-APR-1998.
 XX 10-OCT-1997; 97NO-EP05614.
 XX 16-OCT-1996; 96EP-0870131.
 XX 09-SEP-1997; 97EP-0870133.
 XX (INNO-) INNOGENETICS NV.
 XX (DDL-) DDL BV.
 XX Quint W, Van Doorn L;
 XX WPI; 1998-251300/22.

XX Method for detecting and/or typing Helicobacter pylori strains -
 XX comprises use of primers and probes based on vacA and caga gene
 XX Claim 19; Figure 12; 122pp; English.

XX This invention describes a novel method for the detection and/or typing
 XX of Helicobacter pylori strains present in a sample using PCR primers and
 XX probes to detect regions of the vacuolating toxin (vaca) gene and other

CC virulence determinant genes (VDG) e.g. the cytotoxin-associated (caga)
 CC gene. The method allows the typing and allele-specific detection of a
 CC strain according to the VDG alleles present in that particular H. pylori
 CC strain. The virulence determinant genes are the genetic elements
 CC involved in enabling, determining, and marking the infectivity and/or
 CC pathogenicity of the H. pylori strain. The method provides a way of
 CC detecting H. pylori strains in a sample with respect to the development
 CC of chronic active gastritis, gastric and duodenal ulcers, gastric
 CC adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or
 CC determining eradication therapy. AAV73508-V73546 represent PCR primers
 CC and probes used in the detection of the H. pylori vacA and caga genes.
 CC The primers and probes are used especially to detect the vacA S regions
 CC S1a/b/c and S2 and the M regions M1 and M2 which are represented in
 CC AAV73547-V73785.

XX Sequence 105 BP; 21 A; 29 C; 23 G; 31 T; 1 other;

XX Query Match 93.11; Score 97.8; DB 19; Length 105;
 Best Local Similarity 95.24; Pred. No. 9.8e-23;
 Matches 100; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
 DB 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
 QY 61 TGTGCTCTTTTACAAACCGTGATCATTTCCAGCCATTGTTGGGG 105
 DB 61 TGCGCGCTTTTACAAACCGTGATCATTTCCAGCHATTGTTGGGG 105

RESULT 13
 AAV73642
 ID AAV73642 standard; DNA; 105 BP.
 AC AAV73642;
 XX AAV73642;
 DT 22-MAR-2000 (first entry)
 DE H. pylori vacA S-region s1c DNA fragment 95_20001.

XX PCR primer; probe; vacA; caga; detection; vacuolating toxin; VDG;
 XX virulence determinant gene; cytotoxin-associated gene; allele-specific;
 XX infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer;
 XX adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy;
 XX S region; S1a; S1b; S1c; S2; M region; M1; M2; ss.

XX Helicobacter pylori.

XX WO9816558-A2.
 XX 23-APR-1998.
 XX 10-OCT-1997; 97NO-EP05614.
 XX 16-OCT-1996; 96EP-0870131.
 XX 09-SEP-1997; 97EP-0870133.
 XX (INNO-) INNOGENETICS NV.
 XX (DDL-) DDL BV.

XX Quint W, Van Doorn L;
 XX WPI; 1998-251300/22.

XX Method for detecting and/or typing Helicobacter pylori strains -
 XX comprises use of primers and probes based on vacA and caga gene
 XX Claim 19; Figure 12; 122pp; English.

XX This invention describes a novel method for the detection and/or typing
 XX of Helicobacter pylori strains present in a sample using PCR primers and
 XX probes to detect regions of the vacuolating toxin (vaca) gene and other
 XX virulence determinant genes (VDG) e.g. the cytotoxin-associated (caga)

CC gene. The method allows the typing and allele-specific detection of a
 CC strain according to the VDG alleles present in that particular H. pylori
 CC strain. The virulence determinant genes are the genetic elements
 CC involved in enabling, determining, and marking the infectivity and/or
 CC pathogenicity of the H. pylori strain. The method provides a way of
 CC detecting H. pylori strains in a sample with respect to the development
 CC of chronic active gastritis, gastric and duodenal ulcers, gastric
 CC adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or
 CC determining eradication therapy. AAV73508-V73546 represent PCR primers
 CC and probes used in the detection of the H. pylori vacA and cagA genes.
 CC The primers and probes are used especially to detect the vacA S regions
 CC S1a/b/c and S2 and the M regions M1 and M2 which are represented in
 CC AAV73547-V73785.

XX
 SQ Sequence 105 BP; 20 A; 28 C; 24 G; 33 T; 0 other;

Query Match 92.4%; Score 97; DB 19; Length 105;
 Best Local Similarity 95.2%; Pred. No. 1.8e-22;
 Matches 100; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTGTCAGCATCACACCAAAAAGTCA 60
 DB 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTGTCAGCATCACACCGCAAAAAGTCA 60
 QY 61 TGCTGCTCTTTTACACCGTGATCATTCAGCCATTGTTGGGG 105
 DB 61 TGCCGCTTTTTCACACCGTGATCATTCGCGCCATTGTTGGGG 105

RESULT 14
 AAV73649
 ID AAV73649 standard; DNA; 105 BP.
 XX
 AC AAV73649;
 XX
 DT 22-MAR-2000 (first entry)
 XX
 DE H. pylori vacA S-region s1c DNA fragment NIP2001.
 XX
 KW PCR primer; probe; vacA; cagA; detection; vacuolating toxin; VDG;
 KW virulence determinant gene; cytotoxin-associated gene; allele-specific;
 KW infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer;
 KW adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy;
 KW S region; S1a; S1b; S1c; S2; M region; M1; M2; ss.
 XX
 OS Helicobacter pylori.

XX
 PN WO9816658-A2.
 XX
 PD 23-APR-1998.
 XX
 PF 10-OCT-1997; 97WO-EP05614.
 XX
 PR 16-OCT-1996; 96EP-0870131.
 PR 09-SEP-1997; 97EP-0870133.
 XX
 PA (INNO-) INNOGENETICS NV.
 PA (DDL-) DDL BV.
 XX
 PI Quint. W, Van Doorn L;
 XX
 DR WPI; 1998-251300/22.
 XX

PT Method for detecting and/or typing Helicobacter pylori strains -
 PT comprises use of primers and probes based on vacA and cagA gene
 XX
 PS Claim 19; Figure 12; 122pp; English.

CC This invention describes a novel method for the detection and/or typing
 CC of Helicobacter pylori strains present in a sample using PCR primers and
 CC probes to detect regions of the vacuolating toxin (vacA) gene and other
 CC virulence determinant genes (VDG) e.g. the cytotoxin-associated (cagA)
 CC gene. The method allows the typing and allele-specific detection of a

CC strain according to the VDG alleles present in that particular H. pylori
 CC strain. The virulence determinant genes are the genetic elements
 CC involved in enabling, determining, and marking the infectivity and/or
 CC pathogenicity of the H. pylori strain. The method provides a way of
 CC detecting H. pylori strains in a sample with respect to the development
 CC of chronic active gastritis, gastric and duodenal ulcers, gastric
 CC adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or
 CC determining eradication therapy. AAV73508-V73546 represent PCR primers
 CC and probes used in the detection of the H. pylori vacA and cagA genes.
 CC The primers and probes are used especially to detect the vacA S regions
 CC S1a/b/c and S2 and the M regions M1 and M2 which are represented in
 CC AAV73547-V73785.

XX
 SQ Sequence 105 BP; 20 A; 30 C; 24 G; 31 T; 0 other;

Query Match 92.4%; Score 97; DB 19; Length 105;
 Best Local Similarity 95.2%; Pred. No. 1.8e-22;
 Matches 100; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTGTCAGCATCACACCAAAAAGTCA 60
 DB 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTGTCAGCATCACACCGCAAAAAGTCA 60
 QY 61 TGCTGCTCTTTTACACCGTGATCATTCAGCCATTGTTGGGG 105
 DB 61 TGCCGCTTTTTCACACCGTGATCATTCAGCCATTGTTGGGG 105

RESULT 15
 AAV73652
 ID AAV73652 standard; DNA; 105 BP.
 XX
 AC AAV73652;
 XX
 DT 22-MAR-2000 (first entry)
 XX
 DE H. pylori vacA S-region s1c DNA fragment NIP1001.
 XX
 KW PCR primer; probe; vacA; cagA; detection; vacuolating toxin; VDG;
 KW virulence determinant gene; cytotoxin-associated gene; allele-specific;
 KW infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer;
 KW adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy;
 KW S region; S1a; S1b; S1c; S2; M region; M1; M2; ss.
 XX
 OS Helicobacter pylori.

XX
 PN WO9816658-A2.
 XX
 PD 23-APR-1998.
 XX
 PF 10-OCT-1997; 97WO-EP05614.
 XX
 PR 16-OCT-1996; 96EP-0870131.
 PR 09-SEP-1997; 97EP-0870133.
 XX
 PA (INNO-) INNOGENETICS NV.
 PA (DDL-) DDL BV.
 XX
 PI Quint W, Van Doorn L;
 XX
 DR WPI; 1998-251300/22.
 XX

PT Method for detecting and/or typing Helicobacter pylori strains -
 PT comprises use of primers and probes based on vacA and cagA gene
 XX
 PS Claim 19; Figure 12; 122pp; English.

CC This invention describes a novel method for the detection and/or typing
 CC of Helicobacter pylori strains present in a sample using PCR primers and
 CC probes to detect regions of the vacuolating toxin (vacA) gene and other
 CC virulence determinant genes (VDG) e.g. the cytotoxin-associated (cagA)
 CC gene. The method allows the typing and allele-specific detection of a
 CC strain according to the VDG alleles present in that particular H. pylori

strain. The virulence determinant genes are the genetic elements involved in enabling, determining, and marking the infectivity and/or pathogenicity of the *H. pylori* strain. The method provides a way of detecting *H. pylori* strains in a sample with respect to the development of chronic active gastritis, gastric and duodenal ulcers, gastric adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or determining eradication therapy. AAV73508-V73546 represent PCR primers and probes used in the detection of the *H. pylori* vacA and cagA genes. The primers and probes are used especially to detect the vacA S regions S1a/b/c and S2 and the M regions M1 and M2 which are represented in AAV73547-V73785.

Sequence 105 BP; 21 A; 29 C; 23 G; 32 T; 0 other;

Query Match 92.4%; Score 97; DB 19; Length 105;

Best Local Similarity 95.2%; Pred. No. 1.8e-22;

Matches 100; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

1 CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60

|||||

1 CCCTCTGGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCGCAAAAAAGTCA 60

|||||

61 TGCTGCTTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105

|||||

61 TGCCGCTTCTTTACACCGTGATCATTCAGCCATTGTTGGAGG 105

|||||

Search completed: January 13, 2004, 01:27:30

Job time : 277 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 13, 2004, 01:07:41 ; Search time 61 Seconds
(without alignments)
759.758 Million cell updates/sec

Title: US-10-035-978A-126

Perfect score: 105

Sequence: 1 ccccttagttcttcgctt.....attccagccattgttggggg 105

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/prodata/2/ina/5A COMB.seq:*

2: /cgn2_6/prodata/2/ina/5B COMB.seq:*

3: /cgn2_6/prodata/2/ina/6A COMB.seq:*

4: /cgn2_6/prodata/2/ina/6B COMB.seq:*

5: /cgn2_6/prodata/2/ina/6C COMB.seq:*

6: /cgn2_6/prodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	87.4	83.2	4042	1	US-08-200-232-1
2	87.4	83.2	4042	5	PCT-US95-02219-1
3	87.4	83.2	4042	5	PCT-US95-02219A-1
4	85.8	81.7	3860	3	US-08-470-260-2
5	85.8	81.7	3860	3	US-08-471-491-2
6	85.8	81.7	3860	3	US-08-466-662-2
7	39.4	37.5	1412	2	US-08-295-643-1
8	28.6	27.2	2616	4	US-09-220-132-6
9	27.6	26.3	1001	4	US-09-641-638-387
10	27.6	26.3	1001	4	US-09-641-638-388
11	27.6	26.3	1001	4	US-09-641-638-389
12	27.2	25.9	1665	4	US-09-247-155-72
13	27	25.7	925	1	US-08-850-117-1
14	27	25.7	925	2	US-09-030-5698-1
15	27	25.7	1311	2	US-07-903-103-3
16	25.8	24.6	1710	1	US-08-044-619A-3
17	25.8	24.6	1710	1	US-08-283-911-3
18	25.8	24.6	1710	1	US-08-245-500A-4
19	25.8	24.6	1710	1	US-08-390-546-4
20	25.8	24.6	1710	1	US-08-390-479A-4
21	25.8	24.6	1710	1	US-08-557-393-4
22	25.8	24.6	1710	1	US-08-390-516C-4
23	25.8	24.6	1710	1	US-08-390-517A-4
24	25.8	24.6	1710	1	US-08-390-515A-4
25	25.8	24.6	1710	2	US-08-801-718-4
26	25.8	24.6	1710	3	US-09-073-567-12
27	25.8	24.6	1710	3	US-09-073-567-12

c	28	25.8	24.6	1710	4	US-09-170-159A-4	Sequence 4, Appl
c	29	25.8	24.6	1710	4	US-09-480-718-45	Sequence 45, Appl
c	30	25.6	24.4	162450	4	US-09-345-882-1	Sequence 1, Appl
c	31	25.4	24.2	4065	4	US-09-016-434-1105	Sequence 1105, Ap
c	32	25.4	24.2	4739	3	US-08-685-871-1	Sequence 1, Appl
c	33	25.4	24.2	5596	3	US-09-078-294-5	Sequence 5, Appl
c	34	25.4	24.2	80246	3	US-09-078-294-4	Sequence 4, Appl
c	35	25.4	24.2	80595	3	US-09-078-294-3	Sequence 3, Appl
c	36	25	23.8	948	4	US-09-252-991A-10169	Sequence 10169, A
c	37	25	23.8	2110	1	US-08-416-581B-6	Sequence 6, Appl
c	38	25	23.8	2852	1	US-08-416-581B-7	Sequence 7, Appl
c	39	25	23.8	2852	1	US-08-416-581B-8	Sequence 8, Appl
c	40	25	23.8	2869	1	US-08-369-796-11	Sequence 11, Appl
c	41	25	23.8	2869	2	US-08-852-091-11	Sequence 11, Appl
c	42	25	23.8	2869	2	US-08-820-754-11	Sequence 11, Appl
c	43	25	23.8	2869	3	US-08-956-652-11	Sequence 11, Appl
c	44	25	23.8	2869	3	US-08-956-869-11	Sequence 11, Appl
c	45	25	23.8	2869	3	US-08-948-547-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-200-232-1
; Sequence 1, Application US/08200232
; Patent No. 5721349
; GENERAL INFORMATION:
; APPLICANT: Cover, Timothy L.
; APPLICANT: Blaser, Martin J.
; TITLE OF INVENTION: VACUOLATING TOXIN-DEFICIENT H. PYLORI
; TITLE OF INVENTION: AND RELATED METHODS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG P.C.
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/200,232
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Spratt, Gwendolyn D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 2200.023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4042 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 101..3964
; US-08-200-232-1

Query Match 83.2%; Score 87.4; DB 1; Length 4042;
Best Local Similarity 89.5%; Pred. No. 1e-21;
Matches 94; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY

1 CCCCTTAGTTCTCTCGCTTTAGTGGGGTATTGGTCAGCATCACCCACAAAAGTCA 60

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,260
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/256,848
FILING DATE: 21-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,113
TELEPHONE: (510) 601-2708
TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: 0316.001
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3960 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IS-08-470-260-2

Query Match 81.7%; Score 85.8; DB 3; Length 3960;
Best Local Similarity 88.6%; Pred. No. 3.8e-21;
Matches 93; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
1 CCCTTAGTTCTCTCGCTTTAGTGGGTTATGTCAGCATCACACCAAAAAGTCA 60
53 CCCTCTGGTTCTCTCGCTTTAGTGGGTTATGTCAGCATCACACCGCAACAAAGTCA 112
61 TGCTGCCCTTTTACAACCGTGATCATTCAGCCATTGTTGGGG 105
113 TGCCGCCCTTTTACAACCGTGATCATTCAGCCATTGTTGGGG 157

RESULT 5
IS-08-471-491-2
Sequence 2, Application US/08471491B
Patent No. 6090611
GENERAL INFORMATION:
APPLICANT: Covacci, Antonello
APPLICANT: Bugnoli, Massimo
APPLICANT: Telford, John
APPLICANT: Macchia, Giovanni
APPLICANT: Rappuoli, Rino
TITLE OF INVENTION: Helicobacter Pylori Proteins Useful For Vaccines And
TITLE OF INVENTION: Helicobacter Pylori Proteins Useful For Vaccines And
FILE REFERENCE: CHIR0044
CURRENT APPLICATION NUMBER: US/08/471,491B
CURRENT FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 3960
TYPE: DNA
ORGANISM: Helicobacter pylori
IS-08-471-491-2
Query Match 81.7%; Score 85.8; DB 3; Length 3960;
Best Local Similarity 88.6%; Pred. No. 3.8e-21;
Matches 93; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
1 CCCTTAGTTCTCTCGCTTTAGTGGGTTATGTCAGCATCACACCAAAAAGTCA 60
53 CCCTCTGGTTCTCTCGCTTTAGTGGGTTATGTCAGCATCACACCGCAACAAAGTCA 112
61 TGCTGCCCTTTTACAACCGTGATCATTCAGCCATTGTTGGGG 105
113 TGCCGCCCTTTTACAACCGTGATCATTCAGCCATTGTTGGGG 157

Db 113 TGCCGCCCTTTTACAACCGTGATCATTCAGCCATTGTTGGGG 157
RESULT 6
US-08-466-662-2
Sequence 2, Application US/08466662B
Patent No. 6130059
GENERAL INFORMATION:
APPLICANT: Covacci, Antonello
APPLICANT: Bugnoli, Massimo
APPLICANT: Telford, John
APPLICANT: Macchia, Giovanni
APPLICANT: Rappuoli, Rino
TITLE OF INVENTION: Helicobacter Pylori Proteins Useful For Vaccines And
TITLE OF INVENTION: Helicobacter Pylori Proteins Useful For Vaccines And
FILE REFERENCE: CHIR0057
CURRENT APPLICATION NUMBER: US/08/466,662B
CURRENT FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 3960
TYPE: DNA
ORGANISM: Helicobacter pylori
US-08-466-662-2

Query Match 81.7%; Score 85.8; DB 3; Length 3960;
Best Local Similarity 88.6%; Pred. No. 3.8e-21;
Matches 93; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
1 CCCTTAGTTCTCTCGCTTTAGTGGGTTATGTCAGCATCACACCAAAAAGTCA 60
53 CCCTCTGGTTCTCTCGCTTTAGTGGGTTATGTCAGCATCACACCGCAACAAAGTCA 112
61 TGCTGCCCTTTTACAACCGTGATCATTCAGCCATTGTTGGGG 105
113 TGCCGCCCTTTTACAACCGTGATCATTCAGCCATTGTTGGGG 157

RESULT 7
US-08-295-643-1
Sequence 1, Application US/08295643
Patent No. 5859219
GENERAL INFORMATION:
APPLICANT: COVER, TIMOTHY L.
APPLICANT: BLASER, MARTIN J.
TITLE OF INVENTION: PURIFIED VACUOLATING TOXIN FROM
TITLE OF INVENTION: HELICOBACTER PYLORI AND METHODS TO USE SAME
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESS: NEEDLE & ROSENBERG, P.C.
STREET: Suite 1200, 127 Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,643
FILING DATE: 26-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SPRATT, GWENDOLYN D.
REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 2200.025
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404/688-0770
TELEFAX: 404/688-9880
INFORMATION FOR SEQ ID NO: 1:

```
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1412 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-295-643-1
Query Match 37.5%; Score 39.4; DB 2; Length 1412;
Best Local Similarity 97.6%; Pred. No. 9.3e-05;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 65 GCCTCTTTTACAACCGTGATCATTCAGCCATTGTTGGGGG 105
|||||
Db 1 GCCTTTTACAACCGTGATCATTCAGCCATTGTTGGGGG 41

RESULT 8
US-09-220-132-6/c
; Sequence 6, Application US/09220132
; Patent No. 6506607
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
; OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 07334-074001
; CURRENT APPLICATION NUMBER: US/09/220,132
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/079,303
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: US 60/068,821
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 2616
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-220-132-6

Query Match 27.2%; Score 28.6; DB 4; Length 2616;
Best Local Similarity 59.0%; Pred. No. 0.81;
Matches 49; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 12 CTCCTCGTTTATGCGGTTATGTCAGCATCACACACAAAAGTCATGCTGCTTCT 71
|||||
Db 274 CGCTCTTATCGTTAGACATCTGATCATCATCACACCTCAAAAATTTACTGTTCCCTTCT 215

Qy 72 TTACAACCGTGATCATTCAGCC 94
|||||
Db 214 CCATCATCAAAAATCCAGCC 192

RESULT 9
US-09-641-638-387/c
; Sequence 387, Application US/09641638
; Patent No. 6432648
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
; FILE REFERENCE: GENSET.051CPI
; CURRENT APPLICATION NUMBER: US/09/641,638
; CURRENT FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 388
; LENGTH: 1001
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 501
; OTHER INFORMATION: 12-886-348 : polymorphic base T or C
; NAME/KEY: misc_binding
; LOCATION: 481..500
; OTHER INFORMATION: 12-886-348.misl, potential

Qy 1 CCCTTTAGTTTCTCGCTTTAGTGGGTTATGTCAGCATCACACCAAAAAGT 58
|||||
Db 410 CCTGTCACCTTAGTAGTGAAGTTGGTTATTGTCATAATCATCTCACAAAAGT 353

Query Match 26.3%; Score 27.6; DB 4; Length 1001;
Best Local Similarity 67.2%; Pred. No. 1.3;
Matches 39; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CCCTTTAGTTTCTCGCTTTAGTGGGTTATGTCAGCATCACACCAAAAAGT 58
|||||
Db 410 CCTGTCACCTTAGTAGTGAAGTTGGTTATTGTCATAATCATCTCACAAAAGT 353

RESULT 10
US-09-641-638-388/c
; Sequence 388, Application US/09641638
; Patent No. 6432648
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
; FILE REFERENCE: GENSET.051CPI
; CURRENT APPLICATION NUMBER: US/09/641,638
; CURRENT FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 388
; LENGTH: 1001
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 501
; OTHER INFORMATION: 12-886-348 : polymorphic base T or C
; NAME/KEY: misc_binding
; LOCATION: 481..500
; OTHER INFORMATION: 12-886-348.misl, potential
```

```
;
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 387
; LENGTH: 1001
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 501
; OTHER INFORMATION: 12-886-195 : polymorphic base T or C
; NAME/KEY: misc_binding
; LOCATION: 502..521
; OTHER INFORMATION: 12-886-195.misl, potential complement
; NAME/KEY: misc_binding
; LOCATION: 482..500
; OTHER INFORMATION: 12-886-195.mis2
; NAME/KEY: primer_bind
; LOCATION: 674..694
; OTHER INFORMATION: upstream amplification primer, complement
; NAME/KEY: primer_bind
; LOCATION: 246..266
; OTHER INFORMATION: downstream amplification primer
; NAME/KEY: misc_binding
; LOCATION: 489..513
; OTHER INFORMATION: 12-886-195 potential probe
US-09-641-638-387

Query Match 26.3%; Score 27.6; DB 4; Length 1001;
Best Local Similarity 67.2%; Pred. No. 1.3;
Matches 39; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CCCTTTAGTTTCTCGCTTTAGTGGGTTATGTCAGCATCACACCAAAAAGT 58
|||||
Db 410 CCTGTCACCTTAGTAGTGAAGTTGGTTATTGTCATAATCATCTCACAAAAGT 353

RESULT 10
US-09-641-638-388/c
; Sequence 388, Application US/09641638
; Patent No. 6432648
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
; FILE REFERENCE: GENSET.051CPI
; CURRENT APPLICATION NUMBER: US/09/641,638
; CURRENT FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 388
; LENGTH: 1001
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 501
; OTHER INFORMATION: 12-886-348 : polymorphic base T or C
; NAME/KEY: misc_binding
; LOCATION: 481..500
; OTHER INFORMATION: 12-886-348.misl, potential
```

NAME/KEY: misc binding
LOCATION: 502..521
OTHER INFORMATION: 12-886-348.mis2, potential complement
NAME/KEY: primer bind
LOCATION: 827..847
OTHER INFORMATION: upstream amplification primer, complement
NAME/KEY: primer bind
LOCATION: 399..419
OTHER INFORMATION: downstream amplification primer
NAME/KEY: misc binding
LOCATION: 489..513
OTHER INFORMATION: 12-886-348 potential probe
US-09-641-638-388

Query Match 26.3%; Score 27.6; DB 4; Length 1001;
Best Local Similarity 67.2%; Pred. No. 1.3;
Matches 39; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 1 CCCTTTAGTTTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGT 58
Db 563 CCTGTCACITTAGTAGTGAAGTTGGTTATTGTGCATAATCATCTCACAAAGAAGT 506

RESULT 11
US-09-641-638-389/c
Sequence 389, Application US/09641638
Patent No. 6432648
GENERAL INFORMATION:
APPLICANT: Blumenfeld, Marta
APPLICANT: Bougueleret, Lydie
APPLICANT: Chumakov, Ilya
APPLICANT: Cohen, Annick
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
FILE REFERENCE: GENSET.051CPI
CURRENT APPLICATION NUMBER: US/09/641,638
PRIOR FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
SOFTWARE: Patent.pm
SEQ ID NO 389
LENGTH: 1001
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURES:
NAME/KEY: allele
LOCATION: 501
OTHER INFORMATION: 12-887-201 : polymorphic base G or A
NAME/KEY: misc binding
LOCATION: 481..500
OTHER INFORMATION: 12-887-201.mis1, potential
NAME/KEY: misc binding
LOCATION: 502..521
OTHER INFORMATION: 12-887-201.mis2, potential complement
NAME/KEY: primer bind
LOCATION: 683..701
OTHER INFORMATION: upstream amplification primer, complement
NAME/KEY: primer bind
LOCATION: 184..204
OTHER INFORMATION: downstream amplification primer
NAME/KEY: misc binding
LOCATION: 489..513
OTHER INFORMATION: 12-887-201 potential probe
US-09-641-638-389

Query Match 26.3%; Score 27.6; DB 4; Length 1001;

Best Local Similarity 67.2%; Pred. No. 1.3;
Matches 39; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 1 CCCTTTAGTTTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGT 58
Db 994 CCTGTCACITTAGTAGTGAAGTTGGTTATTGTGCATAATCATCTCACAAAGAAGT 937

RESULT 12
US-09-247-155-72
Sequence 72, Application US/09247155A
Patent No. 6312922
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: Complementary DNAs
FILE REFERENCE: GENSET.021A
CURRENT APPLICATION NUMBER: US/09/247,155A
CURRENT FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/081,563
EARLIER FILING DATE: 1998-04-13
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER FILING DATE: 1998-08-10
EARLIER APPLICATION NUMBER: 60/099,273
EARLIER FILING DATE: 1998-10-04
NUMBER OF SEQ ID NOS: 182
SOFTWARE: Patent.pm
SEQ ID NO 72
LENGTH: 1665
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: CDS
LOCATION: 109..738
NAME/KEY: sig_peptide
LOCATION: 109..405
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 4.5
OTHER INFORMATION: seq LAPGSFLAAVDA/LE
FEATURE:
NAME/KEY: polyA signal
LOCATION: 1633..1638
FEATURE:
NAME/KEY: polyA site
LOCATION: 1650..1665
US-09-247-155-72

Query Match 25.9%; Score 27.2; DB 4; Length 1665;
Best Local Similarity 56.8%; Pred. No. 2.2;
Matches 50; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 14 CTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCATGCTGCCCTTCTTT 73
Db 490 CTCGCGGGCTTTGTGCCAGTGGCCCCCATCTGCACTGCACAAATCAATGCTGCCAACTAT 549
QY 74 ACAACCGTCATCATCCAGCCATTGTTG 101
Db 550 GCGAGTGTGAGACTCCAGCTCTGATTG 577

RESULT 13
US-08-850-117-1/c
Sequence 1, Application US/08850117
Patent No. 5747286
GENERAL INFORMATION:
APPLICANT: Wallis, Niccolò
TITLE OF INVENTION: No. 5747286el Compounds
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,117
FILING DATE: 01-MAY-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9609020.4
FILING DATE: 01-MAY-96
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P31479
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 925 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-08-850-117-1

Query Match 25.7%; Score 27; DB 1; Length 925;
Best Local Similarity 56.0%; Pred. No. 2.1;
Matches 51; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 3 CTTTAGTTCTCGCTTTAGTGGGTTATGTGTCAGCATCACACCAAAAAAGTCATG 62
DB 91 CTTTAAACGGTTGGCATGTTGATGATATGTCACCACTCAAGCAAAATCATAGCAG 32
QY 63 CTGCTCTTTTACACCGTCGATCATTCACG 93
DB 31 CCGTCGACTCCACATCTCTGGTCAAGCTAGC 1

RESULT 14
US-09-008-181-1/c
Sequence 1, Application US/09008181
Patent No. 5919904
GENERAL INFORMATION:
APPLICANT: Wallis, Nicola
TITLE OF INVENTION: No. 5919904el Compounds
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,181
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 95/850,117
FILING DATE: 01-MAY-97
APPLICATION NUMBER: 9609020.4
FILING DATE: 01-MAY-96
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P31479
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 925 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-09-008-181-1
Query Match 25.7%; Score 27; DB 2; Length 925;
Best Local Similarity 56.0%; Pred. No. 2.1;
Matches 51; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 3 CTTTAGTTCTCGCTTTAGTGGGTTATGTGTCAGCATCACACCAAAAAAGTCATG 62
DB 91 CTTTAAACGGTTGGCATGTTGATGATATGTCACCACTCAAGCAAAATCATAGCAG 32
QY 63 CTGCTCTTTTACACCGTCGATCATTCACG 93
DB 31 CCGTCGACTCCACATCTCTGGTCAAGCTAGC 1

RESULT 15
US-08-530-569B-1
Sequence 1, Application US/08530569B
Patent No. 5939526
GENERAL INFORMATION:
APPLICANT: Gaugler, Beatrice
APPLICANT: van den Bynde, Benoit
APPLICANT: Schrier, Peter
APPLICANT: Brouwenstijn, Nathalie
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated RAGE-1 Derived Peptides Which
Complex with HLA-B7 Molecules and Uses Thereof
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: Federal Reserve Plaza, 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,569B
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Gates, Edward R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: L0461/7002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1311 base pairs

TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 S-08-530-569B-1

Query Match 25.7%; Score 27; DB 2; Length 1311;
 Best Local Similarity 62.7%; Pred. NO. 2.4;
 Matches 42; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

14 CTCGCTTTAGTGGGTTATTGTCAGCATCACACCACAAAAAGTCATGCTGCCCTTCTTT 73
 |||||
 338 CCTCTTCTCTGGAGTAATGAATCGGACCAATCTCAAAAAATCCACGATGTCATCGGC 397

74 ACAACCG 80
 |||||
 398 ACACCCG 404

Search completed: January 13, 2004, 02:56:33
 Job time : 64 secs

GenCore version 5.1.6
Copyright (C) 1993 - 2004 Compugen Ltd.

MM nucleic - nucleic search, using sw model

run on: January 13, 2004, 01:22:01 ; Search time 305 Seconds
(without alignments)
1195.490 Million cell updates/sec

file: US-10-035-978A-126

effect score: 105

sequence: 1 cccttagttctctcgctt.....attccagccattgttg9999 105

coring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

searched: 2276164 seqs, 1736306516 residues

total number of hits satisfying chosen parameters: 4552328

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

database : Published Applications NA.*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	105	100.0	105	13	US-10-035-978A-126
2	105	100.0	105	13	US-10-035-978A-126
3	105	100.0	105	13	US-10-035-978A-126
4	105	100.0	105	13	US-10-035-978A-126
5	103.4	98.5	105	13	US-10-035-978A-126
6	103.4	98.5	105	13	US-10-035-978A-126
7	101.8	97.0	105	13	US-10-035-978A-126
8	101.8	97.0	105	13	US-10-035-978A-126
9	100.2	95.4	105	13	US-10-035-978A-126
10	100.2	95.4	105	13	US-10-035-978A-126
11	100.2	95.4	105	13	US-10-035-978A-126
12	100.2	95.4	105	13	US-10-035-978A-126
13	100.2	95.4	105	13	US-10-035-978A-126
14	100.2	95.4	105	13	US-10-035-978A-126
15	99.4	94.7	105	13	US-10-035-978A-126

16	99.4	94.7	105	13	US-10-035-978A-126	Sequence 130, App
17	98.6	93.9	105	13	US-10-035-978A-136	Sequence 136, App
18	98.6	93.9	105	13	US-10-035-978A-137	Sequence 137, App
19	98.6	93.9	105	13	US-10-035-978A-136	Sequence 136, App
20	98.6	93.9	105	13	US-10-035-978A-137	Sequence 137, App
21	98.6	93.9	105	13	US-10-035-978A-137	Sequence 137, App
22	98.6	93.9	105	13	US-10-035-978A-137	Sequence 137, App
23	98.6	93.9	105	13	US-10-035-978A-137	Sequence 137, App
24	98.6	93.9	105	13	US-10-035-978A-137	Sequence 137, App
25	98.6	93.9	105	13	US-10-035-978A-137	Sequence 137, App
26	98.6	93.9	105	13	US-10-035-978A-137	Sequence 137, App
27	98.6	93.9	105	13	US-10-035-978A-137	Sequence 137, App
28	98.6	93.9	105	13	US-10-035-978A-137	Sequence 137, App
29	98.6	93.9	105	13	US-10-035-978A-137	Sequence 137, App
30	98.6	93.9	105	13	US-10-035-978A-137	Sequence 137, App
31	98.6	93.9	105	13	US-10-035-978A-137	Sequence 137, App
32	98.6	93.9	105	13	US-10-035-978A-137	Sequence 137, App
33	98.6	93.9	105	13	US-10-035-978A-137	Sequence 137, App
34	98.6	93.9	105	13	US-10-035-978A-137	Sequence 137, App
35	98.6	93.9	105	13	US-10-035-978A-137	Sequence 137, App
36	98.6	93.9	105	13	US-10-035-978A-137	Sequence 137, App
37	98.6	93.9	105	13	US-10-035-978A-137	Sequence 137, App
38	98.6	93.9	105	13	US-10-035-978A-137	Sequence 137, App
39	98.6	93.9	105	13	US-10-035-978A-137	Sequence 137, App
40	98.6	93.9	105	13	US-10-035-978A-137	Sequence 137, App
41	98.6	93.9	105	13	US-10-035-978A-137	Sequence 137, App
42	98.6	93.9	105	13	US-10-035-978A-137	Sequence 137, App
43	98.6	93.9	105	13	US-10-035-978A-137	Sequence 137, App
44	98.6	93.9	105	13	US-10-035-978A-137	Sequence 137, App
45	98.6	93.9	105	13	US-10-035-978A-137	Sequence 137, App

ALIGNMENTS

RESULT 1
US-10-035-978A-126
Sequence 126, Application US/10035978A
Publication No. US20030165860A1
GENERAL INFORMATION:
APPLICANT: Quint, Wilhelmus
APPLICANT: Van Doorn, Leendert
TITLE OF INVENTION: PROBES, METHODS AND KITS FOR DETECTION
AND TYPING OF HELICOBACTER PYLORI NUCLEIC ACIDS IN
TITLE OF INVENTION: BIOLOGICAL SAMPLES
FILE REFERENCE: INNOG2.001C1
CURRENT APPLICATION NUMBER: US/10/035.978A
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/284,725
PRIOR FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: EP 97870133.2
PRIOR FILING DATE: 1997-09-09
PRIOR APPLICATION NUMBER: EP 96870131.8
PRIOR FILING DATE: 1996-10-16
NUMBER OF SEQ ID NOS: 280
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 126
LENGTH: 105
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Helicobacter pylori vacA nucleic acid sequence
US-10-035-978A-126

Query Match	100.0%	Score 105;	DB 13;	Length 105;
Best Local Similarity	100.0%	Pred. No. 6.8e-28;		
Matches 105;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACACAAAAGTCA	60	
Db	1	CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACACAAAAGTCA	60	
Qy	61	TGCTGCCTTCTTTACACCGTGATCATCCAGCCATTGTTGGGG 105		

```
Db 61 TGTGCGCTTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105
RESULT 2
US-10-035-978a-127
; Sequence 127, Application US/10035978A
; Publication No. US20030165860A1
; GENERAL INFORMATION:
; APPLICANT: Quint, Wilhelmus
; APPLICANT: Van Doorn, Leendert
; TITLE OF INVENTION: PROBES, METHODS AND KITS FOR DETECTION
; TITLE OF INVENTION: AND TYPING OF HELICOBACTER PYLORI NUCLEIC ACIDS IN
; TITLE OF INVENTION: BIOLOGICAL SAMPLES
; FILE REFERENCE: INNOG2.001C1
; CURRENT APPLICATION NUMBER: US/10/035,978A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/284,725
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: EP 97870133.2
; PRIOR FILING DATE: 1997-09-09
; PRIOR APPLICATION NUMBER: EP 96870131.8
; PRIOR FILING DATE: 1996-10-16
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 127
; LENGTH: 105
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Helicobacter pylori vacA nucleic acid sequence
US-10-035-978a-127
Query Match 100.0%; Score 105; DB 13; Length 105;
Best Local Similarity 100.0%; Pred. No. 6.8e-28;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCTTAGTTTCTCTCGCTTTAGTGGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
Db 1 CCCTTAGTTTCTCTCGCTTTAGTGGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
Qy 61 TGTGCGCTTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105
Db 61 TGTGCGCTTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105
RESULT 3
US-10-263-594-126
; Sequence 126, Application US/10263594
; Publication No. US20030175746A1
; GENERAL INFORMATION:
; APPLICANT: Quint, Wilhelmus
; APPLICANT: Van Doorn, Leendert
; TITLE OF INVENTION: PROBES, METHODS AND KITS FOR DETECTION AND
; TITLE OF INVENTION: Typing of Helicobacter pylori nucleic acids in biological
; samples.
; NUMBER OF SEQUENCES: 280
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP
; STREET: 620 Newport Center Drive, 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/263,594
; FILING DATE: 02-Oct-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/284,725
; FILING DATE: <Unknown>
; APPLICATION NUMBER: EP96/870131.8
; FILING DATE: 16-OCT-1996
; APPLICATION NUMBER: PCT/EP97/05614
; FILING DATE: 10-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E.
```

```
; APPLICATION NUMBER: US/09/284,725
; FILING DATE: <Unknown>
; APPLICATION NUMBER: EP96/870131.8
; FILING DATE: 16-OCT-1996
; APPLICATION NUMBER: PCT/EP97/05614
; FILING DATE: 10-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E.
; REFERENCE/DOCKET NUMBER: 34,115
; TELEPHONE: (949) 760-0404
; TELEFAX: (949) 760-9395
; INFORMATION FOR SEQ ID NO: 126:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 126:
US-10-263-594-126
Query Match 100.0%; Score 105; DB 13; Length 105;
Best Local Similarity 100.0%; Pred. No. 6.8e-28;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCTTAGTTTCTCTCGCTTTAGTGGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
Db 1 CCCTTAGTTTCTCTCGCTTTAGTGGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
Qy 61 TGTGCGCTTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105
Db 61 TGTGCGCTTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105
RESULT 4
US-10-263-594-127
; Sequence 127, Application US/10263594
; Publication No. US20030175746A1
; GENERAL INFORMATION:
; APPLICANT: Quint, Wilhelmus
; APPLICANT: Van Doorn, Leendert
; TITLE OF INVENTION: PROBES, METHODS AND KITS FOR DETECTION AND
; TITLE OF INVENTION: Typing of Helicobacter pylori nucleic acids in biological
; samples.
; NUMBER OF SEQUENCES: 280
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP
; STREET: 620 Newport Center Drive, 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/263,594
; FILING DATE: 02-Oct-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/284,725
; FILING DATE: <Unknown>
; APPLICATION NUMBER: EP96/870131.8
; FILING DATE: 16-OCT-1996
; APPLICATION NUMBER: PCT/EP97/05614
; FILING DATE: 10-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E.
```

REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: INN02.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (949) 760-0404
TELEFAX: (949) 760-9395
INFORMATION FOR SEQ ID NO: 127:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 127:
US-10-263-594-127

Query Match 100.0%; Score 105; DB 13; Length 105;
Best Local Similarity 100.0%; Pred. No. 6.8e-28;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2Y 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
1b 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
2Y 61 TGCTGCCTTCTTTACAAACCGTGATCATTCAGCCATTGTTGGGG 105
1b 61 TGCTGCCTTCTTTACAAACCGTGATCATTCAGCCATTGTTGGGG 105

RESULT 5

US-10-035-978A-128
Sequence 128, Application US/10035978A
Publication No. US20030165860A1
GENERAL INFORMATION:

APPLICANT: Quint, Wilhelms
TITLE OF INVENTION: PROBES, METHODS AND KITS FOR DETECTION
TITLE OF INVENTION: AND TYPING OF HELICOBACTER PYLORI NUCLEIC ACIDS IN
TITLE OF INVENTION: BIOLOGICAL SAMPLES
FILE REFERENCE: INN02.001C1
CURRENT APPLICATION NUMBER: US/10/035,978A
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/284,725
PRIOR FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: EP 97870133.2
PRIOR FILING DATE: 1997-09-09
PRIOR APPLICATION NUMBER: EP 96870131.8
PRIOR FILING DATE: 1996-10-16
NUMBER OF SEQ ID NOS: 280
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 128
LENGTH: 105
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Helicobacter pylori vacA nucleic acid sequence

US-10-035-978A-128

Query Match 98.5%; Score 103.4; DB 13; Length 105;
Best Local Similarity 99.0%; Pred. No. 2.6e-27;
Matches 104; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Y 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
1b 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCGCAAAAAAGTCA 60
Y 61 TGCTGCCTTCTTTACAAACCGTGATCATTCAGCCATTGTTGGGG 105
1b 61 TGCTGCCTTCTTTACAAACCGTGATCATTCAGCCATTGTTGGGG 105

RESULT 6

US-10-263-594-128
Sequence 128, Application US/10263594
Publication No. US20030175746A1
GENERAL INFORMATION:
APPLICANT: Quint, Wilhelms
TITLE OF INVENTION: PROBES, METHODS AND KITS FOR DETECTION AND
TYPING OF HELICOBACTER PYLORI NUCLEIC ACIDS IN BIOLOGICAL
SAMPLES.
NUMBER OF SEQUENCES: 280
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP
STREET: 620 Newport Center Drive, 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/263,594
FILING DATE: 02-Oct-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/284,725
FILING DATE: <Unknown>
APPLICATION NUMBER: EP96/870131.8
FILING DATE: 16-Oct-1996
APPLICATION NUMBER: PCT/EP97/05614
FILING DATE: 10-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: INN02.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (949) 760-0404
TELEFAX: (949) 760-9395
INFORMATION FOR SEQ ID NO: 128:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 128:
US-10-263-594-128

Query Match 98.5%; Score 103.4; DB 13; Length 105;
Best Local Similarity 99.0%; Pred. No. 2.6e-27;
Matches 104; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
Db 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCGCAAAAAAGTCA 60
QY 61 TGCTGCCTTCTTTACAAACCGTGATCATTCAGCCATTGTTGGGG 105
Db 61 TGCTGCCTTCTTTACAAACCGTGATCATTCAGCCATTGTTGGGG 105

RESULT 7

US-10-035-978A-132
Sequence 132, Application US/10035978A
Publication No. US20030165860A1
GENERAL INFORMATION:
APPLICANT: Quint, Wilhelms
TITLE OF INVENTION: PROBES, METHODS AND KITS FOR DETECTION
TITLE OF INVENTION: AND TYPING OF HELICOBACTER PYLORI NUCLEIC ACIDS IN

```

; INFORMATION FOR SEQ ID NO: 132:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 105 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 132:
US-10-263-594-132

Query Match          97.0%; Score 101.8; DB 13; Length 105;
Best Local Similarity 98.1%; Pred. No. 9.6e-27;
Matches 103; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
Db 1 CCCTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCGCAAAAAAGTCA 60

Qy 61 TGTGCGCTTCTTTACAAACCGTGATCATTCAGCCATTGTTGGGG 105
Db 61 TGGCGCTTCTTTACAAACCGTGATCATTCAGCCATTGTTGGGG 105

RESULT 9
US-10-035-978A-129
; Sequence 129, Application US/10035978A
; Publication No. US20030165860A1
; GENERAL INFORMATION:
; APPLICANT: Quint, Wilhelmus
; TITLE OF INVENTION: PROBES, METHODS AND KITS FOR DETECTION
; TITLE OF INVENTION: AND TYPING OF HELICOBACTER PYLORI NUCLEIC ACIDS IN
; TITLE OF INVENTION: BIOLOGICAL SAMPLES
; FILE REFERENCE: INNOG2.001C1
; CURRENT APPLICATION NUMBER: US/10/035,978A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/384,725
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: EP 97870133.2
; PRIOR FILING DATE: 1997-09-09
; PRIOR APPLICATION NUMBER: EP 96870131.8
; PRIOR FILING DATE: 1996-10-16
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 129
; LENGTH: 105
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Helicobacter pylori vacA nucleic acid sequence
US-10-035-978A-129

Query Match          95.4%; Score 100.2; DB 13; Length 105;
Best Local Similarity 97.1%; Pred. No. 3.6e-26;
Matches 102; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
Db 1 CCCTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCGCAAAAAAGTCA 60

Qy 61 TGTGCGCTTCTTTACAAACCGTGATCATTCAGCCATTGTTGGGG 105
Db 61 TGGCGCTTCTTTACAAACCGTGATCATTCAGCCATTGTTGGGG 105

RESULT 10
US-10-035-978A-131
; Sequence 131, Application US/10035978A
; Publication No. US20030165860A1
; GENERAL INFORMATION:
; APPLICANT: Quint, Wilhelmus

```

APPLICANT: Van Doorn, Leendert
TITLE OF INVENTION: PROBES, METHODS AND KITS FOR DETECTION
AND TYPING OF HELICOBACTER PYLORI NUCLEIC ACIDS IN
TITLE OF INVENTION: BIOLOGICAL SAMPLES

FILE REFERENCE: INNOG2.001C1
CURRENT APPLICATION NUMBER: US/10/035,978A
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/284,725
PRIOR FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: EP 97870133.2
PRIOR FILING DATE: 1997-09-09
PRIOR APPLICATION NUMBER: EP 96870131.8
PRIOR FILING DATE: 1996-10-16
NUMBER OF SEQ ID NOS: 280
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 131
LENGTH: 105
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Helicobacter pylori vacA nucleic acid sequence
US-10-035-978A-131

Query Match 95.4%; Score 100.2; DB 13; Length 105;
Best Local Similarity 97.1%; Pred. No. 3.6e-26;
Matches 102; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 CCCTTTAGTTCTCTCGCTTTAGTGGGTTATTTGGTCAGCATCACACCAAAAAAGTCA 60
1 CCCTTTAGTTCTCTCGCTTTAGTGGGTTATTTGGTCAGCATCACACCGCAAAAAAGTCA 60

61 TGCTGCTCTTTTACAAACCGTGATCATTCAGCCATTGTTGGGG 105
61 TGCCGCTTCTTTTACAAACCGTGATCATTCGCGCCATTGTTGGGG 105

RESULT 11

US-10-035-978A-133
Sequence 133, Application US/10035978A
Publication No. US20030165860A1

GENERAL INFORMATION:

APPLICANT: Quint, Wilhelmus

APPLICANT: Van Doorn, Leendert

TITLE OF INVENTION: PROBES, METHODS AND KITS FOR DETECTION

AND TYPING OF HELICOBACTER PYLORI NUCLEIC ACIDS IN

TITLE OF INVENTION: BIOLOGICAL SAMPLES

FILE REFERENCE: INNOG2.001C1

CURRENT APPLICATION NUMBER: US/10/035,978A

PRIOR FILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: 09/284,725

PRIOR FILING DATE: 1999-04-16

PRIOR APPLICATION NUMBER: EP 97870133.2

PRIOR FILING DATE: 1997-09-09

PRIOR APPLICATION NUMBER: EP 96870131.8

PRIOR FILING DATE: 1996-10-16

NUMBER OF SEQ ID NOS: 280

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 133

LENGTH: 105

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Helicobacter pylori vacA nucleic acid sequence

US-10-035-978A-133

Query Match 95.4%; Score 100.2; DB 13; Length 105;
Best Local Similarity 97.1%; Pred. No. 3.6e-26;
Matches 102; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 CCCTTTAGTTCTCTCGCTTTAGTGGGTTATTTGGTCAGCATCACACCAAAAAAGTCA 60
1 CCCTTTAGTTCTCTCGCTTTAGTGGGCTATTTGGTCAGCATCACCGCAAAAAAGTCA 60

QY 61 TGCTGCTCTTTTACAAACCGTGATCATTCAGCCATTGTTGGGG 105
Db 61 TGCCGCTTCTTTTACAAACCGTGATCATTCAGCCATTGTTGGGG 105

RESULT 12

US-10-263-594-129

Sequence 129, Application US/10263594

Publication No. US20030175746A1

GENERAL INFORMATION:

APPLICANT: Quint, Wilhelmus

APPLICANT: Van Doorn, Leendert

TITLE OF INVENTION: PROBES, METHODS AND KITS FOR DETECTION AND

TYPING OF HELICOBACTER PYLORI NUCLEIC ACIDS IN BIOLOGICAL

SAMPLES.

NUMBER OF SEQUENCES: 280

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP

STREET: 620 Newport Center Drive, 16th Floor

CITY: Newport Beach

STATE: CA

COUNTRY: USA

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/263,594

FILING DATE: 02-Oct-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/284,725

FILING DATE: <Unknown>

APPLICATION NUMBER: EP96/870131.8

FILING DATE: 16-Oct-1996

APPLICATION NUMBER: PCT/EP97/05614

FILING DATE: 10-Oct-1997

ATTORNEY/AGENT INFORMATION:

NAME: Altman, Daniel E.

REGISTRATION NUMBER: 34,115

REFERENCE/DOCKET NUMBER: INNOG2.001APC

TELEPHONE: (949) 760-0404

TELEFAX: (949) 760-9395

INFORMATION FOR SEQ ID NO: 129:

SEQUENCE CHARACTERISTICS:

LENGTH: 105 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

SEQUENCE DESCRIPTION: SEQ ID NO: 129:

US-10-263-594-129

Query Match 95.4%; Score 100.2; DB 13; Length 105;

Best Local Similarity 97.1%; Pred. No. 3.6e-26;

Matches 102; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 CCCTTTAGTTCTCTCGCTTTAGTGGGTTATTTGGTCAGCATCACACCAAAAAAGTCA 60

1 CCCTTTAGTTCTCTCGCTTTAGTGGGTTATTTGGTCAGCATCACCGCAAAAAAGTCA 60

QY 61 TGCTGCTCTTTTACAAACCGTGATCATTCAGCCATTGTTGGGG 105

Db 61 TGCCGCTTCTTTTACAAACCGTGATCATTCAGCCATTGTTGGGG 105

RESULT 13

US-10-263-594-131

Sequence 131, Application US/10263594

Publication No. US20030175746A1
GENERAL INFORMATION:
APPLICANT: Quint, Wilhelmus
Van Doorn, Leendert
TITLE OF INVENTION: Probes, methods and kits for detection and
typing of Helicobacter pylori nucleic acids in biological
samples.
NUMBER OF SEQUENCES: 280
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP
STREET: 620 Newport Center Drive, 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/263,594
FILING DATE: 02-Oct-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/284,725
FILING DATE: <Unknown>
APPLICATION NUMBER: EP96/870131.8
FILING DATE: 16-OCT-1996
APPLICATION NUMBER: PCT/EP97/05614
FILING DATE: 10-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: INNOG2.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (949) 760-0404
TELEFAX: (949) 760-9395
INFORMATION FOR SEQ ID NO: 131:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 131:
US-10-263-594-131
Query Match 95.4%; Score 100.2; DB 13; Length 105;
Best Local Similarity 97.1%; Pred. No. 3.6e-26;
Matches 102; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CCCTTAGTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
Db 1 CCCTTAGTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCGCAAAAAAGTCA 60
QY 61 TGCTGCCTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105
Db 61 TGCGCGCTTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105
RESULT 14
US-10-263-594-133
Sequence 133, Application US/10263594
Publication No. US20030175746A1
GENERAL INFORMATION:
APPLICANT: Quint, Wilhelmus
Van Doorn, Leendert
TITLE OF INVENTION: Probes, methods and kits for detection and
typing of Helicobacter pylori nucleic acids in biological
samples.
NUMBER OF SEQUENCES: 280

CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP
STREET: 620 Newport Center Drive, 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/263,594
FILING DATE: 02-Oct-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/284,725
FILING DATE: <Unknown>
APPLICATION NUMBER: EP96/870131.8
FILING DATE: 16-OCT-1996
APPLICATION NUMBER: PCT/EP97/05614
FILING DATE: 10-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: INNOG2.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (949) 760-0404
TELEFAX: (949) 760-9395
INFORMATION FOR SEQ ID NO: 133:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 133:
US-10-263-594-133
Query Match 95.4%; Score 100.2; DB 13; Length 105;
Best Local Similarity 97.1%; Pred. No. 3.6e-26;
Matches 102; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CCCTTAGTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
Db 1 CCCTTAGTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCGCAAAAAAGTCA 60
QY 61 TGCTGCCTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105
Db 61 TGCGCGCTTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105
RESULT 15
US-10-035-978A-130
Sequence 130, Application US/10035978A
Publication No. US20030165860A1
GENERAL INFORMATION:
APPLICANT: Quint, Wilhelmus
Van Doorn, Leendert
TITLE OF INVENTION: PROBES, METHODS AND KITS FOR DETECTION
AND TYPING OF HELICOBACTER PYLORI NUCLEIC ACIDS IN
BIOLOGICAL SAMPLES
FILE REFERENCE: INNOG2.001C1
CURRENT APPLICATION NUMBER: US/10/035,978A
FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/284,725
PRIOR FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: EP 97870133.2
PRIOR FILING DATE: 1997-09-09
PRIOR APPLICATION NUMBER: EP 96870131.8
PRIOR FILING DATE: 1996-10-16

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

M nucleic - nucleic search, using sw model

un on: January 13, 2004, 00:39:57 ; Search time 2576 Seconds
(without alignments)
990.672 Million cell updates/sec

itle: US-10-035-978A-126

erfect score: 105

equences: 1 ccccttgattcttcgctt.....attccagccattgttg999g 105

coring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

earched: 22781392 seqs, 12152238056 residues

otal number of hits satisfying chosen parameters: 45562784

inimum DB seq length: 0

aximum DB seq length: 2000000000

ost-processing: Minimum Match 0*

Maximum Match 100*

Listing first 45 summaries

atabase :

EST:*

1: em_estba:*

2: em_estum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hcc:*

9: gb_est1:*

10: gb_est2:*

11: gb_est3:*

12: gb_est4:*

13: gb_est5:*

14: gb_estfun:*

15: em_estom:*

16: em_gss_hum:*

17: em_gss_inv:*

18: em_gss_pln:*

19: em_gss_vrt:*

20: em_gss_fun:*

21: em_gss_mam:*

22: em_gss_mus:*

23: em_gss_pro:*

24: em_gss_rod:*

25: em_gss_phg:*

26: em_gss_vrl:*

27: gb_gss1:*

28: gb_gss2:*

29: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34.2	32.6	691	29	AL234785 Tetraodon
2	32	30.5	549	12	BM085113 saj32d05.
3	31.8	30.3	469	13	BQ294402 1091028H0
4	31.6	30.1	310	10	BE187256 NXNV_76_D

5	31.6	30.1	520	10	BF778904
6	31.6	30.1	528	13	BX253518
7	31.6	30.1	576	13	BQ655776
8	30.8	29.3	1201	9	AL564798
9	30.6	29.1	463	13	BUR32149
10	30.4	29.0	472	14	CA341548
11	30.2	28.8	873	10	BF166498
12	30	28.6	617	13	BUR73870
13	30	28.6	664	12	BI805751
14	30	28.6	671	9	AU091984
15	30	28.6	671	14	CB214094
16	30	28.6	895	29	BZ283602
17	30	28.6	900	11	CNS0818X
18	30	28.6	931	11	CNS09381
19	29.8	28.4	544	12	BM113964
20	29.8	28.4	555	9	AV784009
21	29.8	28.4	583	12	BM067591
22	29.8	28.4	687	12	BQ046120
23	29.8	28.4	796	12	BM113058
24	29.8	28.4	843	29	BZ544215
25	29.8	28.4	1005	10	BG179204
26	29.6	28.2	361	9	AI540803
27	29.6	28.2	401	13	BX105929
28	29.6	28.2	409	9	AI811064
29	29.6	28.2	419	9	AW015371
30	29.6	28.2	451	10	BE553238
31	29.6	28.2	523	14	C83886
32	29.6	28.2	529	13	BU788998
33	29.6	28.2	563	14	CB136036
34	29.6	28.2	566	28	AQ302795
35	29.6	28.2	646	10	BB649562
36	29.6	28.2	649	12	BM678344
37	29.6	28.2	665	12	BQ016353
38	29.6	28.2	668	12	BM684898
39	29.6	28.2	669	13	BQ109548
40	29.6	28.2	671	14	BY729222
41	29.6	28.2	708	14	CA423815
42	29.6	28.2	751	14	CB244690
43	29.6	28.2	815	29	BX169335
44	29.6	28.2	934	14	CA978254
45	29.6	28.2	3127	11	BC015800

ALIGNMENTS

RESULT 1

CNS03A5K/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

CNS03A5K 691 bp DNA linear GSS 01-SEP-2000
Tetraodon nigroviridis genome survey sequence T7 end of clone
008P02 of library G from Tetraodon nigroviridis, genomic survey
sequence.

AL234785

AL234785.1 GI:7893920

GSS; genome survey sequence.

Tetraodon nigroviridis

Tetraodon nigroviridis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetraodontidae; Tetraodontidae; Tetraodon.

1

Roest Crollius.H., Jaillon.O., Dasilva.C., Bouneau.L., Fisher.C.,

Bernot.A., Fizames.C., Wincker.P., Brottier.P., Quetier.F.,

Saurin.W. and Weissenbach.J.

Estimate of human gene number provided by genome-wide analysis

using Tetraodon nigroviridis DNA sequence

Nat. Genet. 25 (2), 235-238 (2000)

20296633

10835645

2

Roest Crollius.H., Jaillon.O., Dasilva.C., Ozouf-Costaz.C.,

Fizames.C., Fischer.C., Bouneau.L., Billault.A., Quetier.F.,

TITLE Saurin, W., Bernot, A. and Weissenbach, J.
JOURNAL Characterization and repeat analysis of the compact genome of the
MDLINE freshwater pufferfish Tetraodon nigroviridis
PUBMED Genome Res. 10 (7), 939-949 (2000)
REFERENCE 20359837
AUTHORS 3 (bases 1 to 691)
TITLE Genoscope.
JOURNAL Direct Submission
 Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
COMMENT - Web : www.genoscope.cns.fr
 This sequence is a single read and was generated as part of a large
 scale clone-end sequencing project of the Tetraodon nigroviridis
 genome. For more information, please take a look at
 http://www.genoscope.cns.fr/tetraodon.

FEATURES

source

1. .691
 Location/Qualifiers
 /organism="Tetraodon nigroviridis"
 /mol_type="genomic DNA"
 /db_xref="taxon:99883"
 /clone="008P02"
 /note="Genoscope sequence ID : COBG008DH01LPL1-end : T7"
BASE COUNT 213 a 132 c 120 g 226 t
ORIGIN

Query Match 32.6%; Score 34.2; DB 29; Length 691;
 Best Local Similarity 67.6%; Pred. No. 1;
 Matches 48; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 4 TTTAGTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAGTCATGC 63
 |||||
Db 687 TTTAATTGACTCCGCTGCTGATTATTGAGCAGCATCAGACCAAAAAGTCACCG 628
 |||||
QY 64 TGCCTCTTTA 74
 |||||
Db 627 AGCAGGCTCTA 617

RESULT 2
BM085113
LOCUS sa32d05.y1 Gm-cl066 Glycine max cDNA clone SOYBEAN CLONE ID:
DEFINITION Gm-cl066-4401.5' similar to SW:LOX4_SOYBN P38417 LIPOXYGENASE-4 ;
 mRNA sequence.

ACCESSION BM085113
VERSION BM085113.1 GI:16995741
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.

1 (bases 1 to 549)
 Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna
 A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
 Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers
 X., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk
 R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
 R., Waterston, R. and Wilson, R.
 Public Soybean EST Project

TITLE

JOURNAL

COMMENT

Contact: Shoemaker R/Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available through: ResGen, Invitrogen Corp. 2130
 South Memorial Parkway Huntsville, AL 35801 For further information

FEATURES

source

1. .549
 Location/Qualifiers
 /organism="Glycine max"
 /mol_type="mRNA"
 /db_xref="taxon:3847"
 /clone="SOYBEAN CLONE ID: Gm-cl066-4401"
 /tissue_type="Leaf and shoot tip, salt stressed, 2 week
 old seedling"
 /lab_host="DH10B"
 /clone_lib="Gm-cl066"
 /note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
 XhoI; The cDNA library was constructed from mRNA isolated
 from unexpanded leaves and the shoot tips of 2 week old
 seedling from the cultivar Williams. The 2 week old
 seedlings were salt stressed in a solution of 500mM NaCl
 for 3 days prior to harvesting. Complementary DNA was
 synthesized from mRNA using a primer consisting of a
 poly(dT) sequence with a XhoI restriction site. EcoRI
 adapters were ligated to the blunt-ended cDNA fragments
 followed by XhoI digestion. The cDNA fragments were
 directionally cloned into the EcoRI-XhoI restriction site
 of the pBluescript vector. The ligated cDNA fragments were
 transformed into DH10B host cells (GibcoBRL). This library
 was constructed in the laboratory of Dr. Randy
 Shoemaker."

BASE COUNT 173 a 106 c 114 g 156 t
ORIGIN

Query Match 30.5%; Score 32; DB 12; Length 549;
 Best Local Similarity 56.7%; Pred. No. 5.3;
 Matches 59; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 2 CCTTTAGTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAGTCAT 61
 |||||
Db 187 CATTGGTTTCTCTAATCTAGTGGTCTCCTGTCAGCAGGCTATCCAAACAGAGT 246
 |||||
QY 62 GCTGCTCTTTTACAAACCGTGATCATTCAGCCATTTGTTGGGG 105
 |||||
Db 247 TGTTCATCTTAGATCACCATGACTATCTCATTCCATATTTGAGG 290
 |||||

RESULT 3
BQ294402
LOCUS BQ294402
DEFINITION 1091028H03.x2 1091 - Immature ear with common ESTs screened by
 Schmidt lab Zea mays cDNA, mRNA sequence.

ACCESSION BQ294402
VERSION BQ294402.1 GI:20803352
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 469)
 Walbot, V.

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
 University
JOURNAL Unpublished
COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 1091028 row: H column: 03.
 Location/Qualifiers
 1. .469
 /organism="Zea mays"

FEATURES

source

1. .469
 Location/Qualifiers
 /organism="Zea mays"

/mol_type="mRNA"
/cultivar="OH43"
/db_xref="taxon:4577"
/tissue_type="Inflorescence meristem - floral organ primordia"
/dev_stage="0.5 cm to 2 cm"
/lab_host="Stratagene XLOR"
/clone_lib="1091 - Immature ear with common ESTs screened by Schmidt lab"
/note="Organ: Immature ear; Vector: pAD-GAL4; Site: 1: EcoRI; Site: 2: XhoI; RNA from library 606 was filtered for common ESTs found in 606."
130 a 127 c 85 g 127 t

ASE COUNT

ORIGIN

Query Match 30.1%; Score 31.8; DB 13; Length 469;
Best Local Similarity 76.5%; Pred. No. 6;
Matches 39; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

41 ATCACCAACAAAAAGTCATGCTGCTTCTTTACACCGTGCATTTCCA 91
|||||

45 ATCACCAACAAAAAGAGAGCTTCTTCGATTCAGAGTAACAAACCA 95
|||||

RESULT 4

BE187256

OCUS

EFINITION NXNV_76 D06 F Nsf Xylem Normal wood Vertical Pinus taeda cDNA clone
NXNV_76 D06 5' similar to Arabidopsis thaliana sequence At1g15690
putative protein see http://mips.gsf.de/proj/thal/db/index.html,
mRNA sequence.

CCESION

BE187256

BE187256.1 GI:8666440

EST.

KEYWORDS

SOURCE

ORGANISM

Pinus taeda (loblolly pine)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus;
Sederoff, R.

Molecular Basis of Wood Formation in the Pine Megagenome

Unpublished

Contact: Sederoff, Ron

Forest Biotechnology

North Carolina State University

840 Main Campus Drive, Centennial Campus, Campus Box 7247, Raleigh,
NC 27695, USA

Tel: 919 515 7800

Fax: 919 515 7801

Email: ron.sederoff@ncsu.edu

Please see http://web.ahc.umn.edu/biodata/nsfpine/ for further
information.

Seq primer: T3.

Location/Qualifiers

1. 310

/organism="Pinus taeda"

/mol_type="mRNA"

/db_xref="taxon:3352"

/clone_lib="NXNV_76 D06"

/note="Vector: Bluescript SK; Site 1: Eco RI; The
sequences contain a 'cDNA adapter' between the EcoRI site
and the start of the EST. The adapter sequence is
'AATTCGGCAGG'."

BASE COUNT

75 a 53 c 78 g 93 t 11 others

ORIGIN

Query Match

Best Local Similarity 30.1%; Score 31.6; DB 10; Length 310;

Matches 58; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

3 CTTAGTTCTCTCGCTTTAGTGGGTTATTTGGTCAGCATCACACCAAAAAAGTCATG 62
|||||

Db

Qy

Db

RESULT 5

BF778904

LOCUS

DEFINITION

Pinus taeda (loblolly pine)

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

27 CATTTGCTCTACCTGTCATTTTGGAGCCTTTTGTGAGCGTGTGTCAGCGTGTGCAATTCAAACTGTGG 86
|||||

63 CTGCTTTCTTTACCAACCGTATTCATTCAGCATTTGTTGGGG 104
|||||

87 ATGCTTAACCAACCAAAAGTGTTCATTTGTTAAATTTGTTGGG 128
|||||

BF778904 520 bp mRNA linear EST 07-MAY-2003
NXSI_089 G03 F NXSI (Nsf Xylem Side wood Inclined) Pinus taeda cDNA
clone NXSI_089 G03 5' similar to Arabidopsis thaliana sequence
At1g15690 Putative protein see
http://mips.gsf.de/proj/thal/db/index.html, mRNA sequence.

BF778904

BF778904.1 GI:12126804

EST.

Pinus taeda (loblolly pine)

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

Pinus taeda

FEATURES

source

1. 520

/organism="Pinus taeda"

/mol_type="mRNA"

/strain="Coastal plain loblolly pine from North Carolina"

/db_xref="taxon:3352"

/clone="NXSI_089 G03"

/tissue_type="Xylem"

/cell_type="Side"

/dev_stage="Juvenile"

/lab_host="XLI-Blue"

/clone_lib="NXSI (Nsf Xylem Side wood Inclined)"

/note="Vector: Bluescript SK; Site 1: Eco RI; Site 2: XhoI
; The library is from early (spring) wood, taken from
three six-year old trees (three different genotypes), in
the juvenile phase. These trees were induced to form side
wood by bending to a 45 degree angle and tying them to the
ground. Differentiating xylem was harvested from the sides
of the inclined stems, and a mixture of all three
genotypes was used for the library. oligo-dr primed cDNA
was directionally cloned into the EcoRI-XhoI Bluescript SK
vector arms. NOTE: The sequences contain a 'cDNA adapter'
between the EcoRI site and the start of the EST. The
adapter sequence is 'AATTCGGCAGG'."

BASE COUNT

124 a 101 c 135 g 140 t 20 others

ORIGIN

Query Match

Best Local Similarity 30.1%; Score 31.6; DB 10; Length 520;

Matches 58; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

3 CTTAGTTCTCTCGCTTTAGTGGGTTATTTGGTCAGCATCACACCAAAAAAGTCATG 62
|||||

193 CATTTGTTCTCTCGCTTTAGTGGGTTATTTGGTCAGCATCACACCAAAAAAGTCATG 252
|||||

63 CTGCTTTCTCTCGCTTTAGTGGGTTATTTGGTCAGCATCACACCAAAAAAGTCATG 104
|||||

```

Db 253 ATGCTTTACACCAAAAGTGTTCATTGGTTA.TTTTGTGGG 204

RESULT 6
BX253518 528 bp mRNA linear EST 24-FEB-2003
LOCUS
DEFINITION BX253518 Pinus pinaster differentiating xylem adult Pinus pinaster
          cDNA clone PP084E10 similar to PYROPHOSPHATE ENERGIZED VACUOLAR
          MEMBRANE PROTON PUMP, mRNA sequence.
ACCESSION BX253518
VERSION BX253518.1 GI:28520427
KEYWORDS
SOURCE
ORGANISM Pinus pinaster
          Pinus pinaster
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE 1 (bases 1 to 528)
AUTHORS Canton,F.R., Le Provost,G., Garcia,V., Barre,A., Frigerio,J.-M.,
          Paiva,J., Fevereiro,P., Avila,C., Mouret,J.-F., Brach,J., de
          Daruvar,A., Canovas,F.M. and Plomion,C.
TITLE Transcriptional analysis of wood formation in maritime pine
JOURNAL Unpublished
COMMENT Contact: Frigerio JM
          Genetique et Amelioration 69
          INRA
          route d'Arcachon 33612 Cestas CEDEX France
          Email: Frigerio@pierrotton.inra.fr
          Email: Frigerio@pierrotton.inra.fr.
FEATURES
          source
          1. 528
              /organism="Pinus pinaster"
              /mol_type="mRNA"
              /strain="ecotype: Corsican"
              /db_xref="taxon:71647"
              /clone="PP084E10"
              /tissue_type="differentiating xylem"
              /dev_stage="adult"
              /note="Lib="Pinus pinaster differentiating xylem adult"
              RI, Site 2: Xho I; A composite cDNA library was made with
              mRNA isolated from normal, compression, opposite, early
              and late wood of Maritime pine uni-directionally cloned
              into Uni-ZAP XR using the ZAP-cDNA Synthesis kit
              (Stratagene). pBluescript SK(-) plasmids were obtained by
              in vivo mass excision. The nucleotide sequence of the
              5'end was obtained by automated sequencing with the T3
              primer by GENOME EXPRESS, Meylan, France"
          130 a 106 c 141 g 151 t

Query Match 30.1%; Score 31.6; DB 13; Length 528;
Best Local Similarity 56.9%; Pred. No. 7.2;
Matches 58; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Qy 3 CTTTGTCTCTCGCTTGTAGTGGGTTATTGTCAGCATCACACCAAAAAAGTCATG 62
    |||||
Db 211 CATTGGTGTCATTGCACTTGTGGAGCCTTCGTGACCGTGTGCAATTCAAACTGTG 270
    |||||

Qy 63 CTGCTTCTTTACACCGTGATCATTCACGCCATTGTTGGG 104
    |||||
Db 271 ATGCTTTACACCAAAAGTGTTCATTGGTTAATTGTTGGG 312
    |||||

RESULT 7
BQ655776 576 bp mRNA linear EST 07-MAY-2003
LOCUS
DEFINITION NXR099_B05_F NXRV (Nsf Xylem Root wood Vertical) Pinus taeda cDNA
          clone NXR099_B05_5' similar to Arabidopsis thaliana sequence
          At1g15690 putative protein see
          http://mips.gsf.de/proj/thal/db/index.html, mRNA sequence.
ACCESSION BQ655776
VERSION BQ655776.1 GI:21788102
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
          Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT On Feb 16, 2001 this sequence version replaced gi:12915562.
          Contact: Genoscope
          Genoscope - Centre National de Sequencage

```

[illegible][illegible]

REFERENCES
AUTHORS

Clark, M., Johnson, S. L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wyllie, T., Underwood, K., Stepcoe, M., Theising, B., Allen, M., Bowers, Y., Parson, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

WashU Zebrafish EST Project 1998

Unpublished

Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

TITLE
JOURNAL
COMMENT

4434 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@wustl.edu

CDNA Library Preparation: Raymond Lee. cDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone Distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
ResourcenZentrumPrimaDatenbank, Berlin, Germany (web address:
www.rzpd.de)

Seq primer: T7 from Gibco
High quality sequence stop: 394.
Location/Qualifiers
1. .472

FEATURES
source

```

/seq_type="nucwa"
/db_xref="taxon:7955"
/sex="mixed male and female"
/tissue_type="3 day fin regenerates"
/lab_host="E. coli XL04"
/clone_lib="zebrafish fin day3 regeneration"
/notes="vector: pBK-CMV; Site 1: EcoRI; Site 2: XhoI; last strand cDNA primed with (GA)10ACTAGTCTCGAG(T)18, followed by second strand synthesis, and ligated to 5' adapter (5')-aattcgccagcag-3', 3'-gccctctc-5'. cDNA was cloned directionally (EcoRI/XhoI) into Stratagene zap express lambda phage arms. Mass in vivo excision done to obtain inserts in pBK-CMV phagemid."
202 a 80 C 78 g 112 t

```

Query Match 29.0%; Score 30.4; DB 14; Length 472;

Best Local Similarity 63.9%; Pred. No. 18;
Matches 46; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 CCCTTTAGTTCTCTCGCTTAGTGGGGTTATGGTCAGCATCACACCAAAAAAGTCA 60
Do 73 CTCCTTATTGTTTGGCTTTTTCATTTTATGTAAGAGTCACATAATAAACTGTGA 14

QY 61 TGTGCGCTCTT 72
Db 13 TGATGCCATTT 2

RESULT 11
BF166498/c
LOCUS
DEFINITION 601774993F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3995615 5', mRNA linear EST 30-OCT-2000
ACCESSION
VERSION BF166498.1 GI:11046850
KEYWORDS
SOURCE
ORGANISM Mus musculus (house mouse)

REFERENCE
AUTHORS 1 (bases 1 to 873)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9215 row: 1 column: 24
High quality sequence stop: 641.
Location/Qualifiers
1. .873
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:3995615"
/tissue_type="spontaneous tumor, metastatic to mammary. Stem cell origin."
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu29"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT 221 a 195 c 237 g 220 t

ORIGIN
Query Match 28.8%; Score 30.2; DB 10; Length 873;
Best Local Similarity 58.2%; Pred. No. 25;
Matches 53; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 9 TTTCTCTCGTTTAGTGGGGTTATGGTCAGCATCACACCAAAAAAGTCATGCT 68
Db 455 TTTAACTACAGTTCCTGTATGTTGTGTGACCCACACCATGAAATTATCCACTGCT 396

QY 69 TCTTTACACCGTGATCATTCAGCCATTGT 99
Db 395 ACTTTAACTGTAATGTTGTGCTACTGTTAT 365

RESULT 12
BU873870
LOCUS
DEFINITION Q060H01 Populus flower cDNA library Populus balsamifera subsp. trichocarpa cDNA 5 prime, mRNA sequence.
ACCESSION
VERSION BU873870.1 GI:24065394
KEYWORDS
SOURCE
ORGANISM Populus balsamifera subsp. trichocarpa
Populus balsamifera subsp. trichocarpa
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids
; eurosids 1; Malpighiales; Salicaceae; Populus.
1 (bases 1 to 617)
Unneberg, P., Bhaller, R.R., Jansson, S. and Sterky, F.
The poplar tree transcriptome: Analysis of expressed sequence tags from multiple libraries
Unpublished
Contact: BHALLERAO RUPALI R.
Umea Plant Science Center
Department of Plant Physiology
University of Umea, 901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: rupali.bhaller@plantphys.umu.se.
Location/Qualifiers
1. .617
/organism="Populus balsamifera subsp. trichocarpa"
/mol_type="mRNA"
/sub_species="trichocarpa"
/db_xref="taxon:3694"
/clone_lib="Populus flower cDNA library"
/note="Organ: flower"

BASE COUNT 140 a 131 c 165 g 181 t

ORIGIN
Query Match 28.6%; Score 30; DB 13; Length 617;
Best Local Similarity 55.9%; Pred. No. 26;
Matches 57; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 3 CTTTAGTTCTCTCGCTTAGTGGGGTTATGGTCAGCATCACACCAAAAAAGTCATG 62
Db 356 CTCCTGTTCCCTTGTGTTTGTGCTTTGTTCAGCAGGGCTGGATCAATCTGTCG 415

QY 63 CTGCTTCTTTACAAACCGTGATCATTCAGCCATTGTTGGGG 104
Db 416 ATGCTTGACCCCTAAGCTCTCATTTGGGCTGATTTGGGG 457

RESULT 13
BU805751/c
LOCUS
DEFINITION S047C04 Stem library from Oryza sativa (3-5 leaf stage) Oryza sativa cDNA clone S047C04, mRNA sequence.
ACCESSION
VERSION BU805751
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 664)
Dong, H.T., Li, D.B., Zhuang, X.F., Dai, C.G., Sun, L.X., Pei, Y.X., Wu, H.F., Jiang, Y.X., Yu, F.C., Gao, Q.K. and Lou, Y.C.
A Gene Expression Screen in Oryza sativa
Unpublished
Contact: Dong HT
Laboratory of Functional Genetics
Bio-technology Institute of Zhejiang University
Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
Tel: 0086-571-86892051
Fax: 0086-571-86961525
Email: htdong@zjuem.zju.edu.cn
Seq primer: M13 forward primer.
Location/Qualifiers

```

source
1. .664
/organism="Oryza sativa"
/mol_type="mRNA"
/db_xref="taxon:4530"
/clone="S047C04"
/tissue_type="Stem"
/dev_stage="3-5 leaf stage"
/clone_lib="Stem library from Oryza sativa (3-5 leaf stage)"
"
/note="Vector: pSport2"
192 a 167 c 138 g 167 t
BASE COUNT
ORIGIN
Query Match 28.6%; Score 30; DB 12; Length 664;
Best Local Similarity 59.3%; Pred. No. 27;
Matches 51; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
y 4 TTTAGTTCTCTCGCTTTAGTGGGGTTATGGTCAGCATCACACCAAAAAAGTCATGC 63
b 211 TTTCTTGATGTCCTCGAAGTGGCGGTATTCAGGTCATCAGCACAAACAGCTATGATCT 152
y 64 TGCCTTCTTTACACCGTGATCATTC 89
b 151 TGTGATCTTTCTCACCCCTGATCAATC 126
RESULT 14
LOCUS AU091984.1 671 bp mRNA linear EST 03-APR-2002
DEFINITION AU091984 Rice root Oryza sativa (japonica cultivar-group) cDNA
ACCESSION AU091984
VERSION AU091984.1 GI:8404630
KEYWORDS EST.
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
Sasaki, T. and Yamamoto, K.
Rice cDNA from root (2000)
Unpublished
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
Tel.: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/
PROJECT "RGP".
FEATURES
Location/Qualifiers
1. .671
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="R0240"
/clone_lib="Rice root"
/note="Prepared from seedling root."
196 a 169 c 136 g 168 t 2 others
BASE COUNT
ORIGIN
Query Match 28.6%; Score 30; DB 9; Length 671;
Best Local Similarity 59.3%; Pred. No. 27;
Matches 51; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
y 4 TTTAGTTCTCTCGCTTTAGTGGGGTTATGGTCAGCATCACACCAAAAAAGTCATGC 63
b 215 TTTCTTGATGTCCTCGAAGTGGCGGTATTCAGGTCATCAGCACAAACAGCTATGATCT 156
y 64 TGCCTTCTTTACACCGTGATCATTC 89

```

```

Db 155 TGTGATCTTTCTCACCCCTGATCAATC 130
RESULT 15
LOCUS CB214094.1 671 bp mRNA linear EST 05-FEB-2003
DEFINITION OML04374 Oryza minuta HybrizAP-2.1 XR library Oryza minuta cDNA 5',
mRNA sequence.
ACCESSION CB214094
VERSION CB214094.1 GI:28260185
KEYWORDS EST.
SOURCE Oryza minuta
ORGANISM Oryza minuta
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
Shin, J.S.
Oryza minuta HybrizAP-2.1 XR library
Unpublished
Contact: Jeong Sheop Shin
Plant Molecular Genetics
Graduate School of Biotechnology, University of Korea
136-701 Anam-dong 5/1 Seoul, Korea
Tel: 00 82 2 3290 3430
Fax: 00 82 2 927 9028
Email: jsshin@kucn.korea.ac.kr.
FEATURES
Location/Qualifiers
1. .671
/organism="Oryza minuta"
/mol_type="mRNA"
/db_xref="taxon:63629"
/dev_stage="4-weeks after germination"
/clone_lib="Oryza minuta HybrizAP-2.1 XR library"
/note="Organ: immature leaf"
181 a 152 c 160 g 178 t
BASE COUNT
ORIGIN
Query Match 28.6%; Score 30; DB 14; Length 671;
Best Local Similarity 59.3%; Pred. No. 27;
Matches 51; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
y 4 TTTAGTTCTCTCGCTTTAGTGGGGTTATGGTCAGCATCACACCAAAAAAGTCATGC 63
b 391 TTTCTTGATGTCCTCGAAGTGGCGGTATTCAGGTCATCAGCACAAACAGCTATGATCT 332
y 64 TGCCTTCTTTACACCGTGATCATTC 89
b 331 TGTGATCTTTCTCACCCCTGATCAATC 306
Search completed: January 13, 2004, 02:55:22
Job time : 2584 secs

```